GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2004, 20:09:36 ; Search time 5876 Seconds
(without alignments)
4772.455 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2		3453	100.0	1944	6	AX825703	AX825703 Sequence
3		3453	100.0	2189	6	AX825705	AX825705 Sequence
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ALIGNMENTS

RESULT 1

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DEFINITION  Sequence 1 from Patent WO0114563.
ACCESSION   AX088876
VERSION     AX088876.1  GI:13397639
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
  AUTHORS   Goring,D. and Silva,N.
  TITLE     Proline-rich extensin-like receptor kinases
  JOURNAL   Patent: WO 0114563-A 1 01-MAR-2001;
            Goring, Daphne (CA) ; Silva, Nancy (CA)
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ORIGIN

Alignment Scores:
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Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-086-464-2 (1-647) x AX088876 (1-1944)

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DEFINITION Sequence 1 from Patent WO03072763.
ACCESSION AX825703
VERSION AX825703.1 GI:39751230
KEYWORDS .
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
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REFERENCE 1
AUTHORS Goring,D., Silva,N. and Haffani,Y.Z.
TITLE Increasing plant seed production
JOURNAL Patent: WO 03072763-A 1 04-SEP-2003;
Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)

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ORIGIN

Alignment Scores:

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Percent Similarity:	100.00%	Conservative:	0
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US-10-086-464-2 (1-647) x AX825703 (1-1944)

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Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360

Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440

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Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

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Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520

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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540

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DEFINITION  Sequence 3 from Patent WO03072763.
ACCESSION   AX825705
VERSION     AX825705.1  GI:39751232
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 3 04-SEP-2003;
            Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
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Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-086-464-2 (1-647) x AX825705 (1-2189)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20

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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40

Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60

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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100

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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120

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Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

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ACCESSION AY028699
VERSION AY028699.1 GI:13447448
KEYWORDS .
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
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REFERENCE 1 (bases 1 to 2189)
AUTHORS Silva,N.F. and Goring,D.R.
TITLE Characterization of a novel Brassica napus receptor protein kinase PERK1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2189)
AUTHORS Silva,N.F. and Goring,D.R.
TITLE Direct Submission
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ORIGIN

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US-10-086-464-2 (1-647) x AY028699 (1-2189)

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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
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Db       1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Db       1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Db       1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Db       1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Db       1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
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Db       2017 GGTTATAGTGGACCTTCTCTT 2037

RESULT 5
AX825738
LOCUS       AX825738               1959 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 36 from Patent WO03072763.
ACCESSION   AX825738
VERSION     AX825738.1  GI:39751255
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1
  AUTHORS  Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE    Increasing plant seed production
  JOURNAL  Patent: WO 03072763-A 36 04-SEP-2003;
           Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES             Location/Qualifiers
     source          1. .1959
                     /organism="Arabidopsis thaliana"
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ORIGIN

Alignment Scores:
Pred. No.:                1.23e-63      Length:          1959
Score:                    2936.50       Matches:         574
Percent Similarity:       90.61%        Conservative:    24
Best Local Similarity:    86.97%        Mismatches:      41
Query Match:              85.04%        Indels:          21
DB:                       6             Gaps:            12

US-10-086-464-2 (1-647) x AX825738 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db          1 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 60

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||    ||||||   |||||||||
Db         61 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 120

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||
Db        121 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 180

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              ||||||   ||||||||||||||||||          |||             ||||||
Db        181 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT------------CCTCCT 228

Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
Db        229 CTTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 285

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||         |||:::||||||          |||||||||:::   ||||||
Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Db        343 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 399

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::|||||||||||||||||||||||||||||||||||||      |||:::|||
Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
              ||||||||||||   |||:::||||||||||||:::   |||||||||   |||||||||
Db        580 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 639

Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
              |||||||||   ||||||||||||   ||||||||||||||:::|||||||||||||||
Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
              ||||||||   ||||||||||||||||||||||||||||||||||||   |||||||||
Db        697 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 756

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 816

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 876

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        877 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 936

Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Db        937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 996

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
              ||||||||||||||||||||:::|||||||||:::||||||   :::||||||||||||||
Db        997 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1056

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
              ||||||||||||||||||||||||||||||||   ||||||||||:::||||||||||||||
Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
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Db       1117 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1176

Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
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Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
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Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Db       1297 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1356

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
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Db       1357 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1416

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
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Db       1417 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1476

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
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Db       1477 GACTGGGCACGACCATTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGAGGGTTTGGCT 1536

Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
              |||:::||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db       1537 GATTCAAAGATGGGTAATGAGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1596

Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
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Db       1597 GCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1656

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
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Db       1657 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1716

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
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Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
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Db       1777 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1836

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Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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Db       1897 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 1956

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BT008400
LOCUS       BT008400                1959 bp    mRNA    linear   PLN 15-MAY-2003
DEFINITION  Arabidopsis thaliana At3g24550 gene, complete cds.
ACCESSION   BT008400
VERSION     BT008400.1  GI:30725473
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     The discrepancy does not affect the protein sequence.
            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
            Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J.,
            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.23e-63        Length:         1959
Score:                  2936.50         Matches:        574
Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x BT008400 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
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              |||         |||:::||||||           |||||||||:::   ||||||
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Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Db        343 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 399

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Qy      408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
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Qy      428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Qy      608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
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DEFINITION  Arabidopsis thaliana protein kinase-like protein mRNA, complete
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ACCESSION   AY128792
VERSION     AY128792.1  GI:22136227
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            The RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Tripp,M.,
            Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R.,
            Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H.,
            Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Tripp,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
            to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford) contributed equally to this work as PIs.
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                     HLVSLIGYCMAGVQRLLVYEFVPNNNLEFHLHGKGRPTMEWSTRLKIALGSAKGLSYL
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                     EGLADSKMGNEYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGM
                     RPGHSNVYSSYGGSTDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPSG
                     SSSEGQATREMEMGKIKKTGQGYSGPSL"
ORIGIN

Alignment Scores:
Pred. No.:              1.29e-63        Length:         2098
Score:                  2936.50         Matches:        574
Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x AY128792 (1-2098)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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  ORGANISM  Arabidopsis thaliana
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
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            Davis,R.W., Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis cDNA clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2116)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
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            Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
            Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L.,
            Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
            Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
            Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
            Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S.,
            Davis,R.W.,  Theologis,A., and Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES              Location/Qualifiers
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ORIGIN

Alignment Scores:
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Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x AY056788 (1-2116)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db         37 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 96

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db         97 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 156

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427

Db       1273 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTTCTGATACA 1332

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RESULT 9
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VERSION     AY059901.1  GI:16649062
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
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REFERENCE   1  (bases 1 to 2188)
  AUTHORS   Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
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            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2001) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
            Southwick,A., Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
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ORIGIN

Alignment Scores:
Pred. No.:              1.33e-63        Length:         2188
Score:                  2936.50         Matches:        574
Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x AY059901 (1-2188)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
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Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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VERSION AY093065.1 GI:20260331
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SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2190)
AUTHORS Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick,A., Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

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ORIGIN

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Best Local Similarity:	86.97%	Mismatches:	41
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US-10-086-464-2 (1-647) x AY093065 (1-2190)

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  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
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            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
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            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
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            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              1.37e-63        Length:         1959
Score:                  2934.50         Matches:        573
Percent Similarity:     90.61%          Conservative:   25
Best Local Similarity:  86.82%          Mismatches:     41
Query Match:            84.98%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x BT008409 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Db        937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 996

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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Db        997 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1056

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
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Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
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Db       1117 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1176

Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
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Db       1177 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1236

Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
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Db       1237 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTTCTGATACA 1296

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Db       1297 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1356

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
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Db       1357 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1416

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
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Db       1417 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1476

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
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Db       1477 GACTGGGCACGACCATTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGAGGGTTTGGCT 1536

Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
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Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
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Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
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Db       1717 GTATACAGCTCATATGGAGGAAGCACAGACTATGACACGAGCCAATACAACGACGACATG 1776

Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
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Db       1777 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1836

Qy        608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
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Db       1837 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1896

Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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Db       1897 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 1956
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RESULT 12
AF370509
LOCUS AF370509 2257 bp mRNA linear PLN 30-APR-2001
DEFINITION Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA, complete cds.
ACCESSION AF370509
VERSION AF370509.1 GI:13877616
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2257)
AUTHORS Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="III"
                     /clone="RAFL11-07-N23"
                     /ecotype="Columbia"
                     /note="This clone is in pBluescript"
     gene            1. .2257
                     /gene="MOB24.13"
     CDS             107. .2065
                     /gene="MOB24.13"
                     /codon_start=1
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                     /protein_id="AAK43886.1"
                     /db_xref="GI:13877617"
                     /translation="MSTAPSPGTTPSPSPPSPPTNSTTTTPPPAASSPPPTTTPSSPP
                     PSPSTNSTSPPPSSPLPPSLPPPSPPGSLTPPIPQPSPSAPITPSPPSPTTPSNPRSP
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                     LCKKKRRRRHDDEAAYYVPPPPPSGPKAGGPYGGQQQYWQQQNASRPSDNHVVTSLPP
                     PKPPSPPRKPPPPPPPPAFMSSSGGSDYSDLPVLPPPSPGLVLGFSKSTFTYEELSRA
                     TNGFSEANLLGQGGFGYVHKGILPSGKEVAVKQLKAGSGQGEREFQAEVEIISRVHHR
                     HLVSLIGYCMAGVQRLLVYEFVPNNNLEFHLHGKGRPTMEWSTRLKIALGSAKGLSYL
                     HEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFGYLAPE
                     YAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEEGDF
                     EGLADSKMGNEYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGM
                     RPGHSNVYSSYGGSTDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPSG
                     SSSEGQATREMEMGKIKKTGQGYSGPSL"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.52e-63 | Length: | 2257 |
| Score: | 2934.50 | Matches: | 573 |
| Percent Similarity: | 90.61% | Conservative: | 25 |
| Best Local Similarity: | 86.82% | Mismatches: | 41 |
| Query Match: | 84.98% | Indels: | 21 |
| DB: | 8 | Gaps: | 12 |

US-10-086-464-2 (1-647) x AF370509 (1-2257)

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Qy   1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
              ||||||:::|||||||||||||||||| ||||||||||||||||||:::
Db   107 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 166

Qy   18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Db   167 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 226

Qy   36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Db   227 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 286

Qy   55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              |||||| |||||||||||||||||||| ||| ||||||
Db   287 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT-----------CCTCCT 334

Qy   75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              :::||||||||||||||| |||||| |||||| |||||||||:::||| |||
Db   335 ATTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 391

Qy   95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              ||| |||:::|||||| |||||||||::: ||||||
Db   392 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 448

Qy   114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
              ||| :::|||||| ||||||::: |||||||||||||| ||||||
Db   449 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 505

Qy   132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db   506 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 565

Qy   152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::||||||||||||||||||||||||||||||||||||| |||:::|||
Db   566 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 625

Qy   170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   626 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 685

Qy   190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Db   686 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 745

Qy   209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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Db        746 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 802

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247

Db        803 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 862

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267

Db        863 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 922

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287

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Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327

Db       1043 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 1102

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347

Db       1103 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1162

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367

Db       1163 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1222

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387

Db       1223 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1282

Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407

Db       1283 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1342

Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427

Db       1343 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTTCTGATACA 1402

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447

Db       1403 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1462

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467

Db       1463 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1522

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487

Db       1523 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1582

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507

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Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527

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Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547

Db       1703 GCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1762

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567

Db       1763 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1822

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587

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Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607

Db       1883 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1942

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Db       2003 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 2062
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RESULT 13
AY089024

LOCUS	AY089024 2324 bp mRNA linear PLN 14-APR-2003
DEFINITION	Arabidopsis thaliana clone 17909 mRNA, complete sequence.
ACCESSION	AY089024
VERSION	AY089024.1 GI:21407798
KEYWORDS	FLI_CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 2324)
AUTHORS	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE	Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE	22088475
PUBMED	12093376
REFERENCE	2 (bases 1 to 2324)
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Full-Length cDNA from Arabidopsis thaliana
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 2324)
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Direct Submission
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES	Location/Qualifiers
source	1. .2324
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	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/clone="17909"

ORIGIN

Alignment Scores:			
Pred. No.:	2.45e-62	Length:	2324
Score:	2885.00	Matches:	570
Percent Similarity:	90.30%	Conservative:	26
Best Local Similarity:	86.36%	Mismatches:	42

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Query Match:          83.55%      Indels:        23
DB:                   8           Gaps:          13

US-10-086-464-2 (1-647) x AY089024 (1-2324)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         18 AsnSerThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Db        165 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 224

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
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Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Db        447 ---GGATCTACTCCTAGAACTCCATCAAACGCTAAACCGTCGCCACCGTCTGATTCTTCC 503

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        504 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 563

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Db        564 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 623

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        624 GCTGCTTACTATGTT---CCTCCTCCTCCTTCTGGTCCCAAAGCTGGAGGACCTTACGGT 680

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
              ||||||||||||   |||:::||||||||||:::   |||||||||   |||||||||
Db        681 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 740

Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
              |||||||||   ||||||||||   ||||||||||||||:::||||||||||||||||
Db        741 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 797

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Db        798 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 857

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
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Db        858 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCAAAAAGCACTTTCACTTATGAGGAG 917

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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RESULT 14
AB020746
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DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24.
ACCESSION   AB020746 BA000014
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            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 3. II.
            Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
            and BAC clones
  JOURNAL   DNA Res. 7 (3), 217-221 (2000)
  MEDLINE   20363099
   PUBMED   10907853
REFERENCE   2  (bases 1 to 79706)
  AUTHORS   Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOB24
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is MXP5 and the 3' clone is MSD24.
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Best Local Similarity:  58.83%          Mismatches:     43
Query Match:            75.93%          Indels:         337
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US-10-086-464-2 (1-647) x AB020746 (1-79706)

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Db      52842 CATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCTGGTAGT 52901

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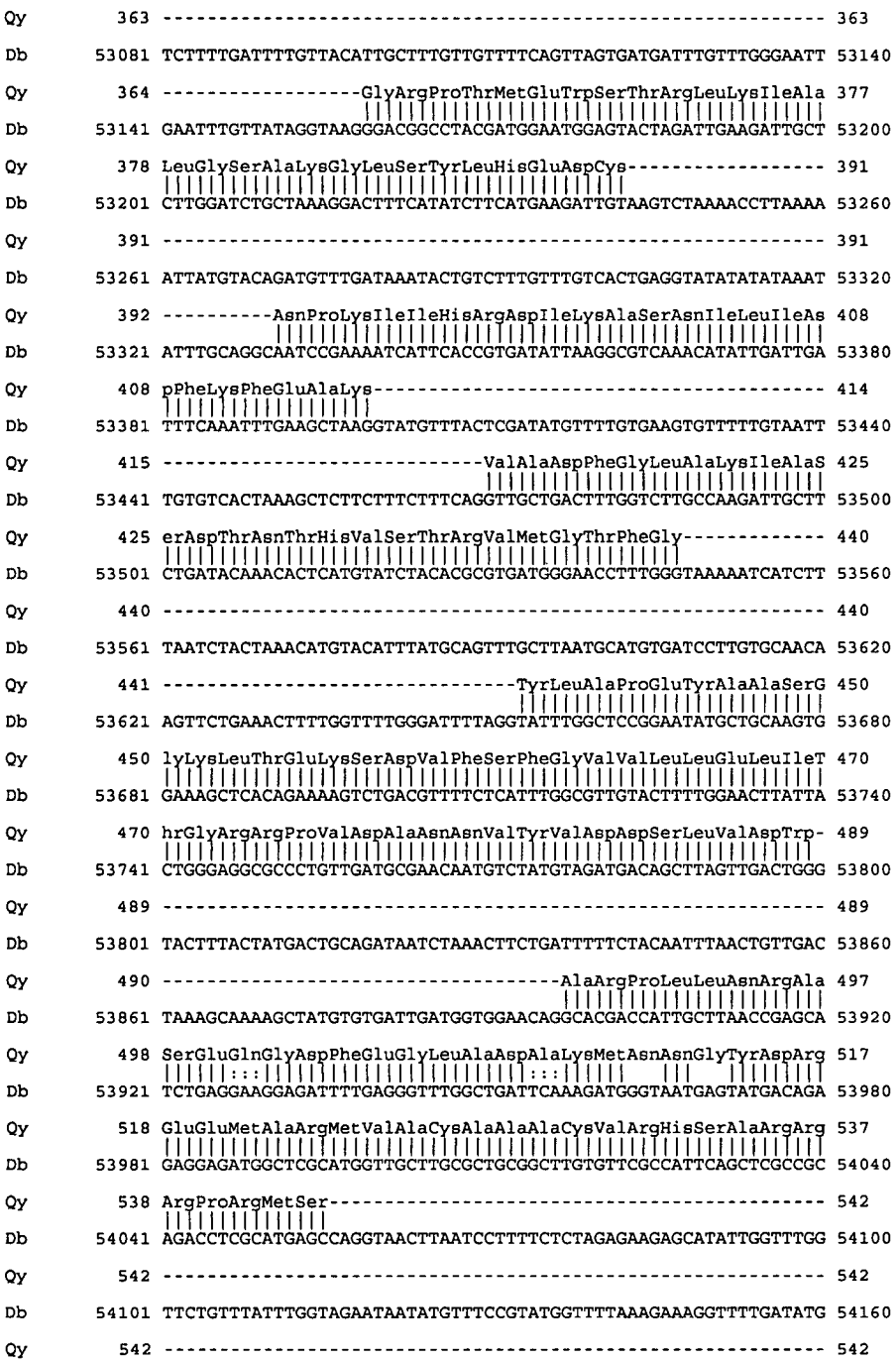

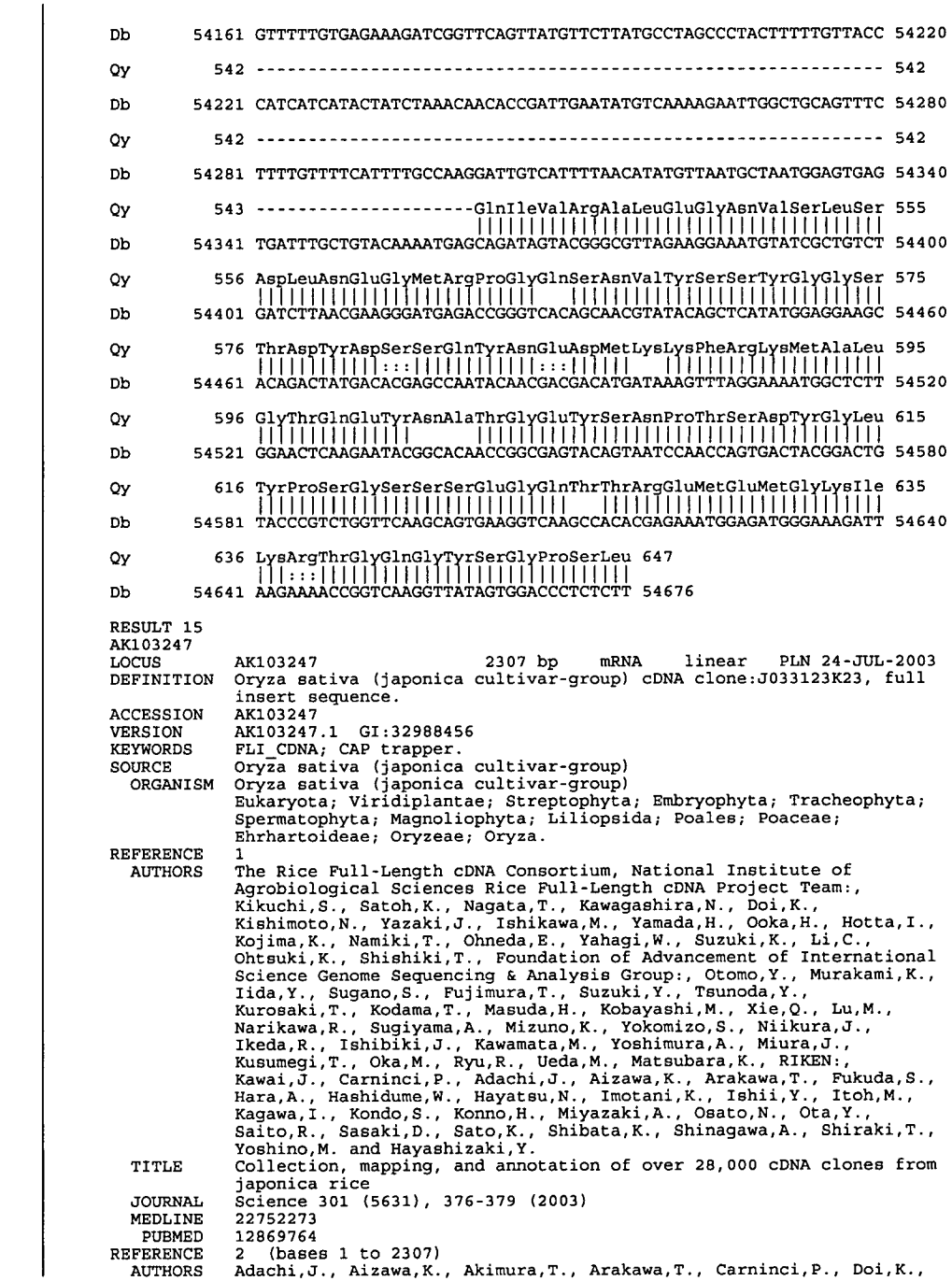

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AK103247
LOCUS       AK103247               2307 bp    mRNA    linear   PLN 24-JUL-2003
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone:J033123K23, full
            insert sequence.
ACCESSION   AK103247
VERSION     AK103247.1  GI:32988456
KEYWORDS    FLI_CDNA; CAP trapper.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   The Rice Full-Length cDNA Consortium, National Institute of
            Agrobiological Sciences Rice Full-Length cDNA Project Team:,
            Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
            Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
            Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
            Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
            Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
            Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
            Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
            Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
            Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
            Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
            Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
            Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
            Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
            Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
            Yoshino,M. and Hayashizaki,Y.
  TITLE     Collection, mapping, and annotation of over 28,000 cDNA clones from
            japonica rice
  JOURNAL   Science 301 (5631), 376-379 (2003)
  MEDLINE   22752273
   PUBMED   12869764
REFERENCE   2  (bases 1 to 2307)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
```

Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

TITLE Direct Submission

JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
source 1. .2307
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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ORIGIN

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Percent Similarity:	64.39%	Conservative:	75
Best Local Similarity:	53.91%	Mismatches:	138
Query Match:	53.33%	Indels:	117
DB:	8	Gaps:	18

US-10-086-464-2 (1-647) x AK103247 (1-2307)

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Qy        3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22
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Qy       23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42
              |||       |||                          :::|||||||||||||||
Db       67 CCCCCTCAGGTCGCA--------------ATCCGCTCCAATTCCCCACCACCACCA--- 108

Qy       43 ThrIleProThrSerProProProSerSerArg-------------------------- 53
                        ||||||||||||      |||
Db      109 -----------TCACCACCGCCGCGAGGGAGAAAAAGCTCTTGCCTGCTCTTTTCTTGG 156

Qy       53 ---------------------------------------------------------- 53

Db      157 CTCCGCTTTGTTCTTGCTCTCATCTTGCTCGTGGCGTGGTAGTCTTCGACTCGTTCTTTT 216

Qy       53 ---------------------------------------------------------- 53

Db      217 TGTTGTTGTTGTTGTTGTGGTGGTGGTGGTGGTGGTAGTGCGTGAGTGAGTGAGTGAGTG 276

Qy       54 ---------SerThrProSerAlaProProProSerProProThrProSerThrProGly 70
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Qy      107 ProProSerAsnProSerArgGluGlyGlySerProArgProProSerSerPro---Ser 125
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Qy      126 ProProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGly 145
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Qy      164 ArgArgArgAspGluGluAspAla--------------------------TyrTyr--- 173
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Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
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Job time : 5988 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2004, 18:28:17 ; Search time 604 Seconds
(without alignments)
4550.636 Million cell updates/sec

Title: US-10-086-464-2
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Scoring table: BLOSUM62
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	3453	100.0	1944	9	ACF36548	Acf36548 B. napus
3	3453	100.0	2189	9	ACF36549	Acf36549 B. napus
4	2936.5	85.0	1959	9	ACF36557	Acf36557 A. thalia
5	2885	83.6	2324	3	AAC36968	Aac36968 Arabidops
6	1821.5	52.8	1812	9	ACF36554	Acf36554 O. sativa
7	1668	48.3	1515	9	ACF36555	Acf36555 Z. mays P
8	1637.5	47.4	1488	9	ACF36556	Acf36556 G. max PE
9	1507	43.6	2520	4	AAF77096	Aaf77096 Arabidops
10	1504	43.6	2520	9	ACF36551	Acf36551 Arabidops
11	1479.5	42.8	2820	4	AAF77097	Aaf77097 Arabidops
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16	1181	34.2	3060	4	AAF77098	Aaf77098 Arabidops
17	839.5	24.3	1923	7	ADA70890	Ada70890 Rice gene
18	816.5	23.6	2124	6	ABZ13274	Abz13274 Arabidops
19	804.5	23.3	2865	7	ADA70701	Ada70701 Rice gene
20	802.5	23.2	2011	4	AAH22557	Aah22557 P. patens
21	797	23.1	1730	7	ADA70647	Ada70647 Rice gene
22	793.5	23.0	2823	7	ADA69478	Ada69478 Rice gene
23	782.5	22.7	1419	3	AAC43029	Aac43029 Arabidops
24	782.5	22.7	1419	6	ABZ13121	Abz13121 Arabidops
25	775.5	22.5	1626	3	AAC48313	Aac48313 Arabidops
26	775.5	22.5	1917	7	ADA70527	Ada70527 Rice gene
27	773	22.4	1479	3	AAC43040	Aac43040 Arabidops
28	769.5	22.3	1353	3	AAC42860	Aac42860 Arabidops
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30	766	22.2	1494	3	AAC48560	Aac48560 Arabidops
31	758.5	22.0	1572	3	AAC42898	Aac42898 Arabidops
32	758.5	22.0	1572	6	ABZ13705	Abz13705 Arabidops
33	758.5	22.0	1920	6	AAL45905	Aal45905 A thalian
34	758.5	22.0	2012	3	AAC44847	Aac44847 Arabidops
35	756	21.9	3239	3	AAA79271	Aaa79271 Eucalyptu
36	754.5	21.9	2136	7	ADA69829	Ada69829 Rice gene
37	749.5	21.7	1751	3	AAC45313	Aac45313 Arabidops
38	744.5	21.6	1485	3	AAC42702	Aac42702 Arabidops
39	740.5	21.4	3525	7	ADA71170	Ada71170 Rice gene
40	740	21.4	2868	3	AAA79266	Aaa79266 Pinus rad
41	740	21.4	3153	7	ADA71066	Ada71066 Rice gene
42	736.5	21.3	1703	3	AAC46629	Aac46629 Zea mays
43	736	21.3	3624	7	ADA69512	Ada69512 Rice gene
44	735	21.3	2004	3	AAC40780	Aac40780 Arabidops
45	734	21.3	1455	3	AAC45877	Aac45877 Arabidops

ALIGNMENTS

RESULT 1
AAF77094
ID AAF77094 standard; DNA; 1944 BP.
XX
AC AAF77094;
XX
DT 17-MAY-2001 (first entry)
XX
DE Brassica napus PERK1 DNA.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Brassica napus.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,

PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Claim 6; Fig 1; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.62e-93	Length:	1944
Score:	3453.00	Matches:	647
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-086-464-2 (1-647) x AAF77094 (1-1944)

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Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Db          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180

Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240

Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Db        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Db        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Db        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

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Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

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Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2
ACF36548
ID   ACF36548 standard; cDNA; 1944 BP.
XX
AC   ACF36548;
XX
DT   18-DEC-2003  (first entry)
XX
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
FH   Key             Location/Qualifiers
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FT                   /transl_except= (pos: 1332. .1334, aa: Phe)
FT                   /product= "PERK1"
FT                   /note= "Proline-rich Extensin-like Receptor Kinase"
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Claim 3; Fig 1A; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.:                4.62e-93        Length:          1944
Score:                    3453.00         Matches:         647
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       9               Gaps:            0

US-10-086-464-2 (1-647) x ACF36548 (1-1944)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Db          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

Qy         21 ThrThrThrProProProAlaSerAlaProProThrThrProSerSerProProPro 40
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Db         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

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Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
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Db       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Db       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
              |||||||||||||||||||||
Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 3
ACF36549
ID   ACF36549 standard; cDNA; 2189 BP.
XX
AC   ACF36549;
XX
DT   18-DEC-2003  (first entry)
XX
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2189
FT                   /*tag=  c
FT                   /note= "ABR82938; this protein contains the amino acids
FT                   corresponding to 5' and 3'UTR regions, though only the
FT                   relevant aa residues (ABR82937) is used in the invention"
FT   5'UTR           1. .96
FT                   /*tag=  a
FT   CDS             97. .2040
FT                   /*tag=  b
FT                   /transl_except= (pos: 1332. .1334, aa: Phe)
FT                   /product= "PERK1"
FT                   /note= "ABR82937; proline-rich Extensin-like Receptor
FT                   Kinase"
FT   3'UTR           2041. .2189
FT                   /*tag=  d
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937, ABR82938.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 1D; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5e-93          Length:        2189
Score:                  3453.00        Matches:       647
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     9              Gaps:          0

US-10-086-464-2 (1-647) x ACF36549 (1-2189)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 156

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Db        1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy         341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db        1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy         361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Db        1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy         401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db        1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy         421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db        1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy         441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Qy         461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Qy         481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Qy         521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Db        1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

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Qy         561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Qy         621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Qy         641 GlyTyrSerGlyProSerLeu 647
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Db        2017 GGTTATAGTGGACCTTCTCTT 2037

RESULT 4
ACF36557
ID   ACF36557 standard; DNA; 1959 BP.
XX
AC   ACF36557;
XX
DT   18-DEC-2003  (first entry)
```

XX
DE A. thaliana PERK1 protein encoding genomic DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 21d; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents an A. thaliana PERK1 DNA (At3g24550)
XX
SQ Sequence 1959 BP; 496 A; 514 C; 425 G; 524 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5.28e-78	Length:	1959
Score:	2936.50	Matches:	574
Percent Similarity:	90.61%	Conservative:	24
Best Local Similarity:	86.97%	Mismatches:	41
Query Match:	85.04%	Indels:	21
DB:	9	Gaps:	12

US-10-086-464-2 (1-647) x ACF36557 (1-1959)

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Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Db         61 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 120

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||||
Db        121 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 180

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              ||||||   ||||||||||||||||||          |||                ||||||
Db        181 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT------------CCTCCT 228

Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
Db        229 CTTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 285

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||         |||:::||||||         |||||||||:::   ||||||
Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
                 |||   :::||||||   ||||||:::      ||||||||||||||   ||||||
Db        343 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 399

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::||||||||||||||||||||||||||||||||||||||      |||:::|||
Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Db        580 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 639

Qy        209 ThrSerLeuProProProProProLysAlaProSerProProArgGlnProProProProPro 228
              |||||||||   ||||||||||||   ||||||||||||||:::|||||||||||||||
Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Db        697 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 756

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
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Db        757 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 816

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Db        817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 876

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        877 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 936

Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 996

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
              ||||||||||||||||||||||||||||||   ||||||||||:::|||||||||||||
Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
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Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1236

Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTTCTGATACA 1296

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1297 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1356

Qy         448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1357 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1416

Qy         468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1417 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1476

Qy         488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
                ||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        1477 GACTGGGCACGACCATTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGAGGGTTTGGCT 1536

Qy         508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
                |||:::||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        1537 GATTCAAAGATGGGTAATGAGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1596

Qy         528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1597 GCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1656

Qy         548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
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Db        1657 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1716

Qy         568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
                ||||||||||||||||||||||||||||||||:::|||||||||||||:::||||||
Db        1717 GTATACAGCTCATATGGAGGAAGCACAGACTATGACACGAGCCAATACAACGACGACATG 1776

Qy         588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
                  ||||||||||||||||||||||||||||||||      ||||||||||||||||
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Qy         608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
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Db        1837 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1896

Qy         628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
                ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        1897 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 1956
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RESULT 5
AAC36968
ID AAC36968 standard; DNA; 2324 BP.
XX
AC AAC36968;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15710.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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Alignment Scores:

Pred. No.:	1.88e-76	Length:	2324
Score:	2885.00	Matches:	570
Percent Similarity:	90.30%	Conservative:	26
Best Local Similarity:	86.36%	Mismatches:	42
Query Match:	83.55%	Indels:	23
DB:	3	Gaps:	13

US-10-086-464-2 (1-647) x AAC36968 (1-2324)

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Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
              ||||||:::||||||||||||||||||          ||||||||||||||||||:::
Db        105 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 164

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||       |||   ||||||   |||||||||
Db        165 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 224

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||
Db        225 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 284

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              ||||||   ||||||||||||||||||          |||              ||||||
Db        285 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT-----------CCTCCT 332

Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
Db        333 CTTCCTCAACCTTCTCCATCCGCTCCCATCACTCCT---TCCCCGCCGTCTCCCACCACA 389

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||       |||:::||||||           |||||||||:::   ||||||
Db        390 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 446

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
                 |||   :::||||||   ||||||:::      ||||||||||||||   ||||||
Db        447 ---GGATCTACTCCTAGAACTCCATCAAACGCTAAACCGTCGCCACCGTCTGATTCTTCC 503

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        504 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 563

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::||||||||||||||||||||||||||||||||||||      |||:::|||
Db        564 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 623
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Qy       170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
Db       624 GCTGCTTACTATGTT---CCTCCTCCTCCTTCTGGTCCCAAAGCTGGAGGACCTTACGGT 680

Qy       190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
Db       681 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 740

Qy       209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
Db       741 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 797

Qy       229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
Db       798 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 857

Qy       248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
Db       858 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCAAAAAGCACTTTCACTTATGAGGAG 917

Qy       268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
Db       918 TTGTCAAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 977

Qy       288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
Db       978 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 1037

Qy       308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
Db      1038 GGGAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 1097

Qy       328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
Db      1098 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCTGATGTTCAAAGATTGCTTGTC 1157

Qy       348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
Db      1158 TATGAGTTTGTTCCTAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGAAGGCCTACA 1217

Qy       368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
Db      1218 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1277

Qy       388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
Db      1278 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1337

Qy       408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
Db      1338 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAGGATTGCTTCTGATACA 1397

Qy       428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
Db      1398 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCAGAATATGCT 1457

Qy       448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
Db      1458 GCAAGCGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGTGTTGTACTTTTGGAG 1517

Qy       468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
Db      1518 CTTATAACCGGGAGGCGCCCTGTTGATGCAAACAATGTCTATGTAGATGACAGCTTAGTT 1577

Qy       488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
Db      1578 GACTGGGCACGACCCTTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGATGGTTTGGCT 1637

Qy       508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
Db      1638 GATTCAAAGATGGGTAATGAGTATAG-AGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1696

Qy       528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
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Db      1697 GCAGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1756

Qy       548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
Db      1757 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1816

Qy       568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
Db      1817 GTATACAGCTCATATGGAGGAAGCACTGACTATGACACGAGCCAATACAACGATGACATG 1876

Qy       588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
Db      1877 AAGAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1936

Qy       608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
Db      1937 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1996

Qy       628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
Db      1997 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 2056
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RESULT 6
ACF36554
ID ACF36554 standard; DNA; 1812 BP.
XX
AC ACF36554;
XX
DT 18-DEC-2003 (first entry)
XX
DE O. sativa PERK protein encoding genomic DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; rice; gene;
KW ds.
XX
OS Oryza sativa.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 21a; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be

```
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents an O. sativa PERK protein encoding genomic DNA (TIGR
CC   Accession No. TC102111)
XX
SQ   Sequence 1812 BP; 409 A; 487 C; 512 G; 404 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.6e-45       Length:          1812
Score:                  1821.50       Matches:         370
Percent Similarity:     71.62%        Conservative:    69
Best Local Similarity:  60.36%        Mismatches:      119
Query Match:            52.75%        Indels:          55
DB:                     9             Gaps:            15

US-10-086-464-2 (1-647) x ACF36554 (1-1812)

Qy         54 SerThrProSerAlaProProProSerProProThrProSerThrProGlySerProPro 73
              |||:::||||||:::|||||||||:::      |||               :::|||||||
Db          4 TCGTCGCCGTCGTCGCCGCCGCCGGCTAACCAGACG-----------GCGACACCGCCT 51

Qy         74 ProLeuProGlnProSer------ProProAlaProThrThrProGlySerProProAla 91
              |||      |||   :::      |||||||||                |||||||||||
Db         52 CCGGCTAACCAGACGGCGGCGCCACCTCCGGCGAGCAACAACTCGTCGTCGCCGCCGGCG 111

Qy         92 Pro------ValThrProProThrArgAsnProProProSerValProGlyProProSer 109
              |||      ::::::||||||:::         ||||||:::   |||   |||||||||
Db        112 CCGGGCTCTTTGTCTCCGCCCTCGCTGACG---CCTCCCGCAGCGCCATCGCCTCCGTCG 168

Qy        110 AsnProSerArgGluGlyGlySerProArgProProSerSerPro---SerProProSer 128
                                                  ||||||||||   :::      :::
Db        169 ACC--------------------------ACGCCCTCCTCGCCGGCGGCGGCGGCGGCG 201

Qy        129 ProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAla 148
              ||||||   ||||||:::|||   ||||||||||||||   :::||||||:::
Db        202 GCGTCGAGCTCGGGGCTGACGACGCCCGTGGTGGTGGGGATCGTGGTGGGCGGCCTCGTC 261

Qy        149 LeuLeuValIleValThr------LeuIleCysLeuLeuCysLysLysLysArgArgArg 166
              :::|||::::::||||||      |||:::||||||      ||||||||||||
Db        262 GTGCTGCTGCTCGTCACCATCCTGCTCGTCTGCCTGTTCAAGAAGAAGAAGCGGCACCAC 321

Qy        167 AspGluGluAspAla--------------------------TyrTyr---------Val 174
                                                       ||||||
Db        322 CACCACCACCCTCCGCCGCCGCCGCCGCCGCACCTCCTGCACTACTACGGCCACCCGCCG 381

Qy        175 ProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGln 194
              ||||||||||||||||||   |||      |||      |||||||||      |||
Db        382 CCGCCGCCGCCGCCCCCGCCGCCGTTCAAAGGGGATCACTATGGTGGGGTGTACCAAAAT 441

Qy        195 TrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProPro 214
              |||:::|||                |||||   |||||||||:::
Db        442 TGGCAGCAAAATGGTCCTCCACCTCCACCTGATCATGTGCTG------------------ 483

Qy        215 ProLysAlaProSerProProArgGlnProProProProProProProProPheMetSer 234
                 |||   ||||||   |||      ||||||||||||   |||               |||
Db        484 AAGAAGGTGCCTTCGCATCCTTCCCCTCCACCACCTCCTGCTCCACTAAATGTACACAGT 543

Qy        235 SerSerGlyGlySerAspTyrSer------------AspArgProValLeuProProPro 250
                    ||||||:::||||||                 :::|||::::::
Db        544 GGTGGTTCTGGCTCAAATTACTCCGGTGGCGACAACAGCCAACCTCTAGTG--------- 594

Qy        251 SerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArg 270
              |||||||||     ||||||||||||:::   ||||||||||||||:::|||:::
Db        595 TCACCTGGTGCTGCATTGGGTTTTTCAAGGTGTACTTTCACTTATGAGGACTTGTCAGCG 654

Qy        271 AlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHis 290
              ||||||:::||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        655 GCGACCGATGGATTCTCCGATGCTAATCTGCTCGGACAGGGCGGTTTTGGGTATGTTCAC 714

Qy        291 LysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGly 310
              ||||||||||||||:::|||   |||||||||||||||||||:::   |||||||||
Db        715 AAAGGAGTTCTGCCGAATGGGACAGAGGTTGCTGTGAAGCAATTGAGAGATGGGAGTGGG 774

Qy        311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        775 CAGGGAGAGCGTGAATTTCAGGCGGAGGTTGAGATTATCAGCCGGGTACATCACAAGCAT 834

Qy        331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
              ||||||:::|||||||||||||||||:::|||   |||||||||||||||||||:::
Db        835 CTTGTAACATTGGTTGGTTATTGCATTTCTGGAGGGAAGAGGTTGCTTGTCTATGAGTAT 894

Qy        351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              ||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        895 GTTCCAAACAACACATTGGAGCTCCACTTGCATGGGAGAGGCCGACCAACCATGGAATGG 954

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
                 |||||||||:::||||||||||:::||||||||||||:::||||||||||||||||
Db        955 CCTACAAGATTACGCATTGCTTTGGGTGCTGCGAAGGGATTGGCATATCTTCATGAAGAT 1014

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::||||||||||||||||||||||||||:::::||||||||:::|||   :::
Db       1015 TGCCATCCTAAGATCATTCACCGTGACATAAAGTCAGCAAATATTCTTCTTGACGCGAGA 1074

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||||||||||||||||||||||||||||||||:::   ||||||   |||||||||
Db       1075 TTTGAGGCAAAGGTGGCAGATTTCGGACTTGCAAAATTGACTTCTGATAATAACACTCAT 1134

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1135 GTTTCAACCAGAGTAATGGGCACATTTGGGTACCTTGCACCAGAGTATGCGTCTTCTGGC 1194

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              :::||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1195 CAGCTAACTGAGAAATCAGATGTCTTTTCTTTCGGAGTAATGCTTCTTGAGCTAATAACT 1254

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||||   :::|||          :::||||||||||||||||||||||||
Db       1255 GGCCGCCGTCCTGTGAGATCGAACCAATCACAGATGGATGACAGCTTGGTTGATTGGGCA 1314

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
              |||||||||:::   |||||||||:::   |||:::::::::   |||   |||   :::
Db       1315 AGGCCTTTAATGATGCGAGCATCAGATGATGGCAATTATGATGCTTTAGTGGATCCACGG 1374

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
              :::          |||:::   ||||||||||||||:::|||||||||||||||||
Db       1375 CTAGGACAGGAGTACAATGGTAACGAGATGGCGAGGATGATTGCTTGTGCAGCTGCTTGT 1434

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGly 550
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db       1435 GTACGCCATTCTGCACGCCGACGCCCACGGATGAGCCAGGTTGTTCGGGCCTTGGAAGGC 1494

Qy        551 AsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSer 570
              :::|||||||||   ||||||||||||||:::|||||||||   |||
Db       1495 GATGTGTCATTGGATGATCTGAACGAAGGTGTTCGTCCTGGCCATAGCCGATTCTTGGGA 1554

Qy        571 SerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPhe 590
              ||||||      |||   :::||||||:::      ||||||||||:::||||||||||
Db       1555 TCATAC---AACAGCAACGAGTACGACACGGGCCATTACAATGAAGACCTGAAGAAATTC 1611

Qy        591 ArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThr 610
              ||||||||||||   |||:::                        |||   |||   |||
Db       1612 AGGAAGATGGCATTTGGCAGTGGCAATCTA------------GAGAGCAGCCAGCAAACG 1659

Qy        611 SerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg------ 628
                                  |||:::   |||   |||   |||          :::
Db       1660 CAGCCCACCGAGTTCGTCCCGAATCGATCCGTATCAATGGGGGATGCGCGTCAAATACCG 1719

Qy        629 ------GluMetGluMetGlyLysIleLysArgThrGly 639
                     ||||||||||||||   :::|||:::   |||
Db       1720 GAGACGGAGATGGAGATGGGGAGTTTGAAGAAAGATGGC 1758

RESULT 7
ACF36555
ID   ACF36555 standard; DNA; 1515 BP.
XX
AC   ACF36555;
XX
```

```
DT   18-DEC-2003  (first entry)
XX
DE   Z. mays PERK protein encoding genomic DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; maize; gene;
KW   ds.
XX
OS   Zea mays.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21b; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR
CC   Accession No. AY108241)
XX
SQ   Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.23e-41      Length:          1515
Score:                  1668.00       Matches:         321
Percent Similarity:     83.87%        Conservative:    43
Best Local Similarity:  73.96%        Mismatches:      59
Query Match:            48.31%        Indels:          12
DB:                     9             Gaps:            4

US-10-086-464-2 (1-647) x ACF36555 (1-1515)

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSer------GlyGly 238
              |||  |||||||||  ||||||||||||      ::::::||||||         |||
Db         26 CCTCCACAGCCGCCAGG-CCACCACCACCAGCGATGCTAAATAGTAGTGCGGGATCTGGT 84

Qy        239 SerAspTyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPhe 258
              |||:::||||||         :::|||||||||||||||||||   ||||||||||||
Db         85 TCTAATTACTCTGGCGGCGAGATCCTACCTCCACCATCCCCTGGAGCTGTTCTTGGCTTC 144

Qy        259 SerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAla 278
              ||||||||||||||||||||||||||||||   |||||||||:::||||||||:::|||
Db        145 TCGAAGAGCACATTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCT 204

Qy        279 AsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLys 298
              |||||||||||||||||||||||||||||||||||||||:::|||:::||||||:::||||||
Db        205 AATCTCCTTGGACAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAA 264

Qy        299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318
              |||:::||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db        265 GAGATTGCTGTAAAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCT 324

Qy        319 GluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338
              ||||||||||||||||||||||||||||||::||||||||||||||||||||||||||||
Db        325 GAGGTTGAGATTATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGC 384

Qy        339 IleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeu 358
              |||:::|||   ||||||||||||||||||||||||||||||||||   ||||||
Db        385 ATTTCTGGAGGCAAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTC 444

Qy        359 HisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeu 378
              |||||||||   :::|||||||||||||||||||||||||      ||||||||||||:::|||
Db        445 CACTTACATGCGAAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTG 504

Qy        379 GlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArg 398
              |||:::|||||||||||||:::|||||||||||||||||||:::|||||||||||||||||||
Db        505 GGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGT 564

Qy        399 AspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPhe 418
              |||||||||||||||||||||||:::||||||:::|||||||||||||||||||||||||
Db        565 GACATAAAGGCATCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGATTTT 624

Qy        419 GlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThr 438
              ||||||||||||      :::|||   ||||||||||||||||||||||||||||||||||||
Db        625 GGACTCGCAAAGTTCACTACTGATAACAACACCCATGTATCGACAAGAGTAATGGGCACC 684

Qy        439 PheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspVal 458
              |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        685 TTTGGGTATTTGGCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTA 744

Qy        459 PheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsn 478
              ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db        745 TTTTCCTTCGGAGTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACC 804

Qy        479 AsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSer 498
                  |||:::|||||||||||||||||||||||||||||||||||||||||   ||||||
Db        805 CAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTT 864

Qy        499 GluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGlu 518
              |||   |||:::::::::  |||   |||   ::::::         ::::::
Db        865 GAGGATGGTGAAATATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAAT 924

Qy        519 GluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArg 538
              ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db        925 GAGATGGCAAGAATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGG 984

Qy        539 ProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsn 558
              |||||||||||||||:::|||||||||||||||||||||||||||||||   |||||||||
Db        985 CCACGTATGAGTCAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAAT 1044

Qy        559 GluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyr 578
              ||||||:::|||||||||   |||       :::   ||||||      |||:::||||||
Db       1045 GAAGGTGTTCGGCCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTAC 1101

Qy        579 AspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGln 598
              ||||||   ||||||||||||||||||||||||||:::|||||||||
Db       1102 GATTCTGGCCAGTACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC 1161

Qy        599 GluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer 618
                        :::   :::||||||   ||||||||:::||||||      ||||||
Db       1162 ------TATACCAGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCT 1215

Qy        619 GlySerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThr 638
              ||||||||||||||||      |||:::|||||||||   |||   :::|||:::
Db       1216 GCATCAAGCAGCGAGGGCCACCAGACGCAAGAGATGGAGTCGGGTGCAATGAAGAAAGGT 1275

Qy        639 Gly-----------------GlnGlyTyrSerGlyProSer 646
              |||                 ||||||||||||   |||
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Db       1276 GGCTACAGTGGTGGCTACAGCTCAGGATACAGCGGAGCCTCG 1317

RESULT 8
ACF36556
ID   ACF36556 standard; DNA; 1488 BP.
XX
AC   ACF36556;
XX
DT   18-DEC-2003  (first entry)
XX
DE   G. max PERK partial EST sequence.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; soybean; gene;
KW   ds.
XX
OS   Glycine max.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21c; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a G. max PERK EST (expressed sequence tag) partial
CC   sequence (TIGR Accession No. TC123698)
XX
SQ   Sequence 1488 BP; 412 A; 291 C; 348 G; 437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.24e-40        Length:         1488
Score:                  1637.50         Matches:        312
Percent Similarity:     89.67%          Conservative:   44
Best Local Similarity:  78.59%          Mismatches:     36
Query Match:            47.42%          Indels:         5
DB:                     9               Gaps:           3

US-10-086-464-2 (1-647) x ACF36556 (1-1488)

Qy        253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272
              |||:::  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GGAATTTCATTGGGGTTCTCTAAGAGCACATTCACGTATGAGGAGTTGGCACGCGCAACT 62

Qy        273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
              :::|||||||||:::|||||||||||||||||||||||||||||||||||||||:::|||
Db         63 GATGGCTTCTCTGATGCCAACCTCCTTGGACAAGGAGGATTTGGATATGTGCACAGAGGA 122

Qy        293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312
              :::||||||:::|||||||||||||||||||||||||||||  ||||||||||||||||
Db        123 ATTCTTCCCAACGGCAAGGAGGTGGCAGTGAAGCAATTGAAGGCTGGAAGCGGGCAAGGG 182

Qy        313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        183 GAGCGTGAATTCCAAGCTGAAGTTGAGATAATTAGCCGTGTCCATCACAAGCATCTTGTT 242

Qy        333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
              ||||||||||||||||||||  |||::::::|||||||||||||||||||||||||||||
Db        243 TCTTTGGTTGGATACTGCATCACTGGGTCCCAGAGGCTGCTTGTTTATGAATTTGTTCCC 302

Qy        353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372
              ||||||  ||||||  ||||||||||||:::|||||||||||||||:::|||  |||
Db        303 AACAACACATTGGAATTCCATTTGCATGGAAAAGGGAGACCTACCATGGATTGGCCCACA 362

Qy        373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
              ||||||:::|||||||||||||||||||||||||:::|||||||||||||||||:::
Db        363 AGACTAAGAATTGCTTTAGGATCTGCTAAGGGACTGGCGTATCTTCATGAAGATTGTCAT 422

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
              ||||||||||||||||||||||||||:::|||||||||:::|||||||||||||||||
Db        423 CCTAAGATCATCCATCGTGATATCAAAGCTGCCAACATCCTTCTGGATTTTAAGTTTGAA 482

Qy        413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
              ||||||||||||||||||||||||||||  :::|||||  ||||||||||||||||
Db        483 GCAAAGGTTGCAGATTTCGGTCTTGCAAAGTTTTCTTCTGATGTCAATACTCATGTTTCT 542

Qy        433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        543 ACTCGAGTGATGGGGACTTTTGGGTATTTGGCTCCAGAATATGCTTCTAGTGGAAAACTG 602

Qy        453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472
              |||:::|||||||||||||||||:::||||||:::|||||||||||||||||||||||||
Db        603 ACAGACAAATCAGATGTTTTCTCCTACGGAGTCATGCTCCTCGAGTTAATAACCGGACGA 662

Qy        473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
              ||||||||||  |||      :::::::::||||||||||||||||||||||||||||
Db        663 CGGCCCGTCGATAAAAATCAAACTTTCATGGAGGATAGTTTGGTAGACTGGGCTAGGCCT 722

Qy        493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
              ||||||  ||||||  |||:::  ||||||:::  :::  |||  ::::::
Db        723 TTGCTCACACGAGCTTTGGAAGAGGATGATTTTGATTCTATTATTGACCCAAGGCTCCAG 782

Qy        513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
              |||  ||||||      ||||||||||||||||||||  ||||||||||:::|||
Db        783 AATGACTATGATCCTAATGAGATGGCACGAATGGTGGCTTCTGCTGCGGCTTGCATACGT 842

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552
              |||||||||:::||||||||||||||||||:::|||||||||||||||||:::|||
Db        843 CATTCGGCAAAGCGTCGACCAAGGATGAGCCAGGTTGTCCGCGCTCTCGAAGGAGATGTC 902

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572
              ||||||:::||||||||||||||:::|||||||||  |||  :::|||||||||:::
Db        903 TCTCTAGCAGATCTGAATGAAGGAATAAGACCTGGACACAGCACTATGTATAGTTCTCAT 962

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592
                  |||:::|||||||||:::::||||||  ||||||||||||||||||||||||
Db        963 ---GAAAGCTCAGATTATGACACTGCACAGTACAAGGAAGACATGAAAAAGTTCAGGAAA 1019

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612
              ||||||||||||||||||||||  |||:::  |||||||||      |||||||:::
Db       1020 ATGGCATTGGGAACTCAGGAGTATGGTGCAAGCAGTGAGTACAGTGCCGCTACAAGTGAG 1079

Qy        613 TyrGlyLeuTyrProSerGlySerSerSerGluGly---------GlnThrThrArgGlu 629
              |||||||||  ||||||||||||||||||||||||          ||||||||||||||
Db       1080 TATGGTTTAAACCCATCAGGCTCAAGTAGTGAAGCACAGAGCCGCCAAACCACAAGGGAA 1139

Qy        630 MetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSer 646
              |||||||||  |||:::|||         ||||||:::|||||||  |||
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Db       1140 ATGGAAATGAGAAAGATGAAG---AACAATCAAGGTTTCAGTGGAAGTTCT 1187

RESULT 9
AAF77096
ID   AAF77096 standard; DNA; 2520 BP.
XX
AC   AAF77096;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Arabidopsis gene #2.
XX
KW   Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200114563-A1.
XX
PD   01-MAR-2001.
XX
PF   18-AUG-2000; 2000WO-CA000966.
XX
PR   19-AUG-1999;   99US-0149466P.
PR   13-OCT-1999;   99US-0159122P.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
XX
PI   Goring D,  Silva N;
XX
DR   WPI; 2001-244305/25.
XX
PT   New proline-rich, extensin-like receptor kinase nucleic acids and
PT   polypeptides useful for increasing plant wounding or pathogen resistance,
PT   or for producing transgenic plants with increased wounding or pathogen
PT   resistance.
XX
PS   Example; Fig 12; 91pp; English.
XX
CC   The present invention relates to proline-rich extensin-like receptor
CC   kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC   increasing the resistance of plants to wounding and pathogens. These are
CC   also useful for producing transgenic plants with increased wounding and
CC   pathogen resistance compared with a wild type plant, as well as in assays
CC   for identifying and developing compounds to inhibit and/or enhance
CC   polypeptide function directly
XX
SQ   Sequence 2520 BP; 717 A; 553 C; 537 G; 713 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.93e-36        Length:         2520
Score:                  1507.00         Matches:        368
Percent Similarity:     53.47%          Conservative:   79
Best Local Similarity:  44.02%          Mismatches:     146
Query Match:            43.64%          Indels:         244
DB:                     4               Gaps:           22

US-10-086-464-2 (1-647) x AAF77096 (1-2520)

Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22
              |||||||||         :::   |||   ||||||||||||||||||::   :::|||
Db         36 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 95

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42
              |||      |||         |||   |||:::   ||||||      ||||||
Db         96 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 146

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62
              :::||||||||||||   |||   |||   |||:::         |||:::
Db        147 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 206

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82
              ||||||      |||:::      ||||||   |||      |||

Db        207 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 263

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102
                  |||:::                |||||||||:::|||    ||||||
Db        264 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 323

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120
              |||         |||||||||      :::   :::   |||      |||       |||
Db        324 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 374

Qy        121 ProSer------------------SerProSerProProSerPro------SerSerAsp 132
              |||                     |||   :::|||||||||          ||||||
Db        375 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 434

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145
              |||                        :::|||   ::::::||||||:::   :::|||
Db        435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 494

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165
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Db        495 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 554

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAla--- 184
                  |||::::::|||       |||   |||       |||
Db        555 -----------GACTCCTTCTAC------CCTGAACCCATGAAAGGTAAAAACATATAC 596

Qy        185 ------------------------------------------------GlyGlyPro 187
                                                              |||
Db        597 ACACTCTTATGTTTCAACAAATAAGAAGCTTAGATTCTTTCATAAAATTTCAGGAAACCA 656

Qy        188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisVal 207
                        :::|||   :::||||||       |||      |||:::
Db        657 ATATCAATACTATGGAAACAACAACAACAACAATGCTTCACAGAATTATCCGAA------ 710

Qy        208 ValThrSerLeuProProProProLysAlaProSerProPro------------------ 221
                  |||   |||             |||   |||
Db        711 ---------TTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGGTTGGGG 761

Qy        222 ArgGln-ProProProProProProProProPheMetSerSerSerGly------GlySe 239
                  |||:::    |||   ||||||||||||||   |||   :::||||||          ||
Db        762 AGGCGGTGGACCATCACCGCCTCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGATTCTTC 821

Qy        239 rAspTyrSer------AspArgProValLeuProProProSerProGlyLeuValLeuGl 257
                  ||||||      |||||||||||||||||||||||||||||||   |||   |||||
Db        822 CATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGCCCTCGG 881

Qy        257 yPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGl 277
                  |||:::|||||||||||||||||:::|||||||||   ||||||   ||||||:::::
Db        882 ATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTTTACGGA 941

Qy        277 uAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGl 297
                  :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 TGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCCTAGCGG 1001

Qy        297 yLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGl 317
                  ||||||||||||||||||   ||||||   ||||||||||||||||||||||||||||
Db       1002 GAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGAGTTTCA 1061

Qy        317 nAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTy 337
                  ||||||||||:::|||||||||||||||||||||||:::|||||||||||||||||||
Db       1062 AGCTGAGGTCGATATCATTAGCCGTGTGCATCATCGGTATCTTGTTTCTTTGGTTGGATA 1121

Qy        337 rCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGl 357
                  ||||||||||      :::|||:::|||||||||||||||||||||      |||||
Db       1122 TTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAACTTTGGA 1181

Qy        357 uLeuHisLeuHisGly------------------------------------------ 362
                  |   ||||||||||||
Db       1182 ATATCATCTTCATGGTTAGACCACTTAAAAACTTTGAGTACTAAGTTTATTTTCTCTAAT 1241

Qy        363 ----------------------------------------Glu-GlyArgProThrM 368
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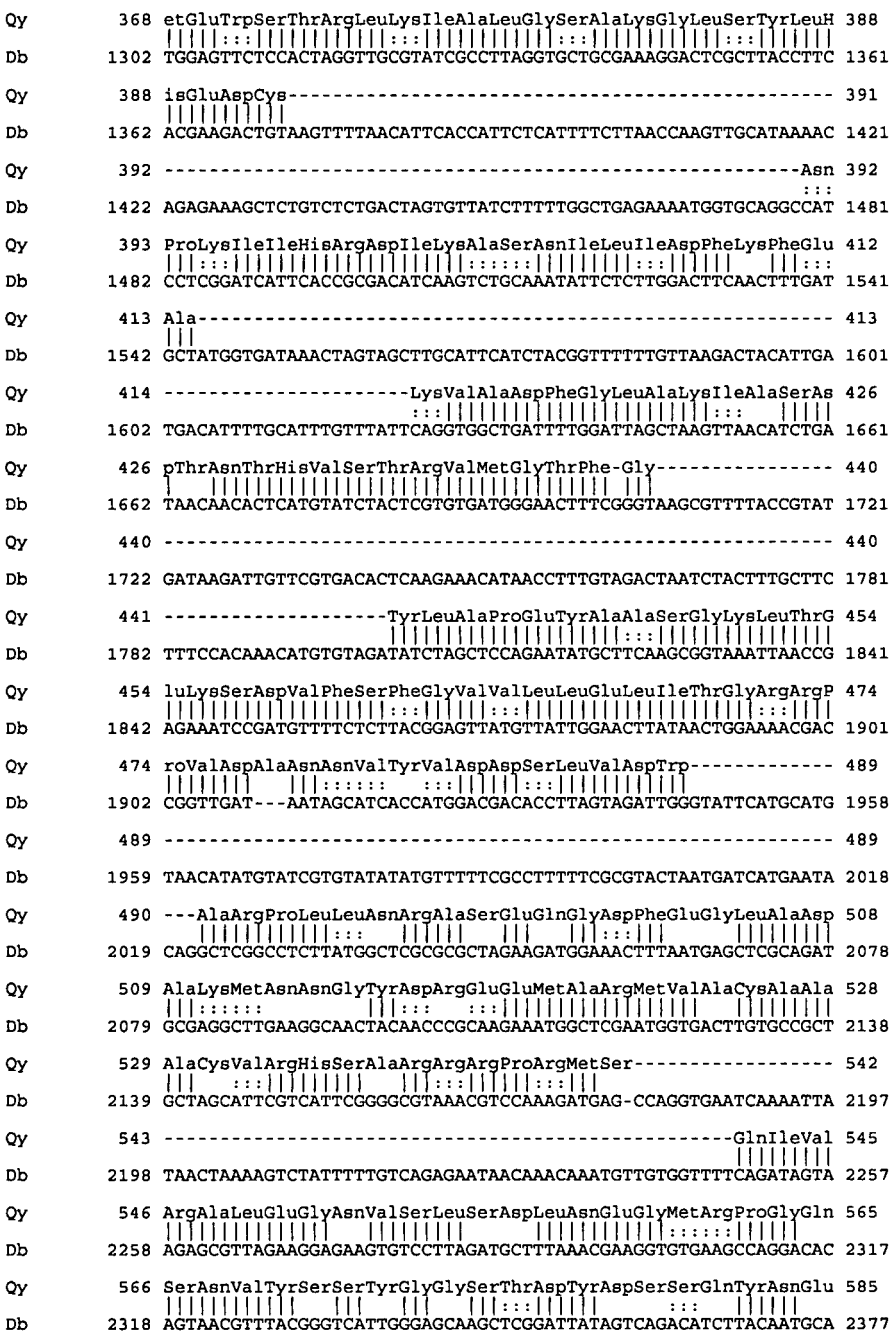
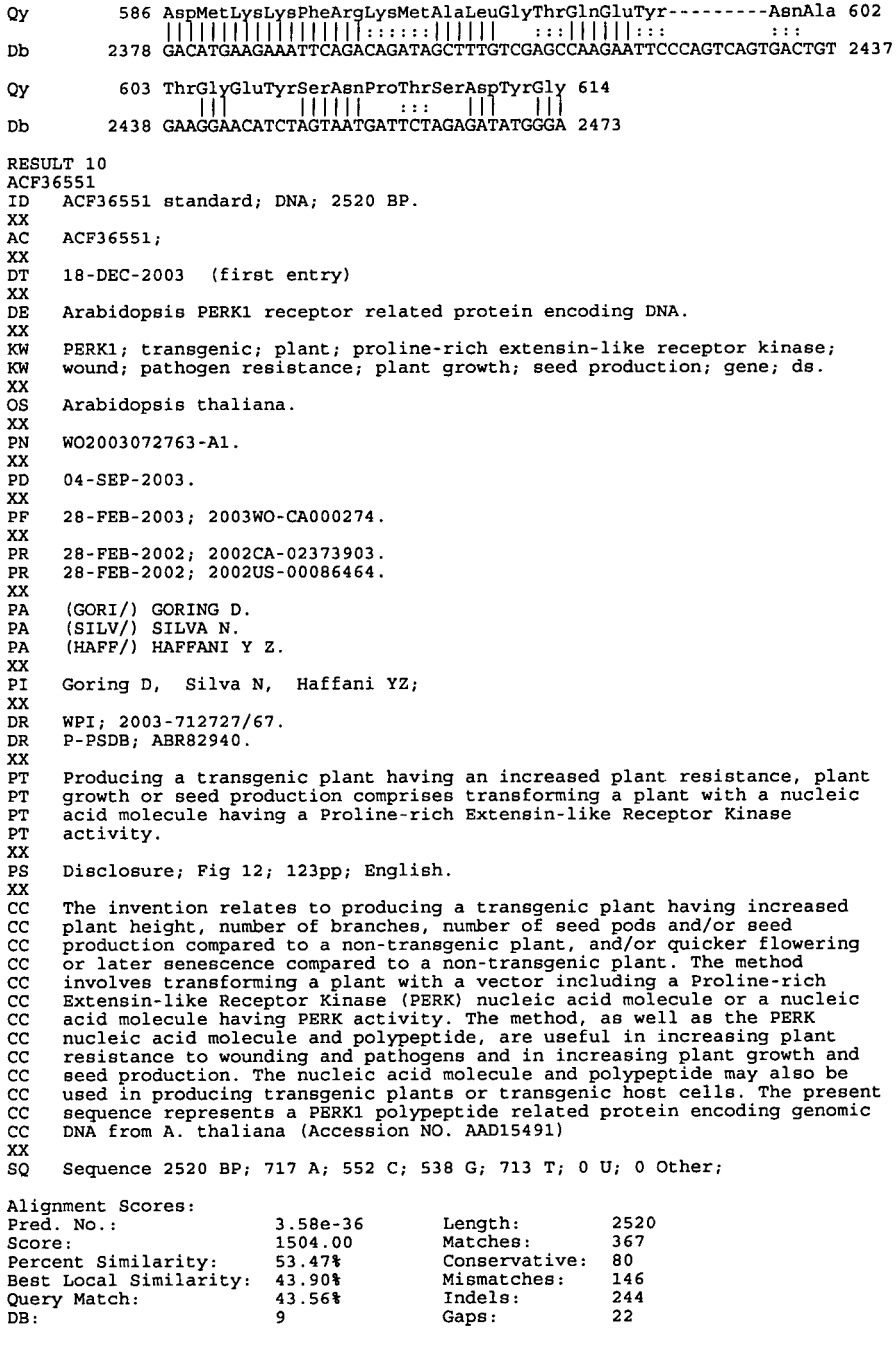


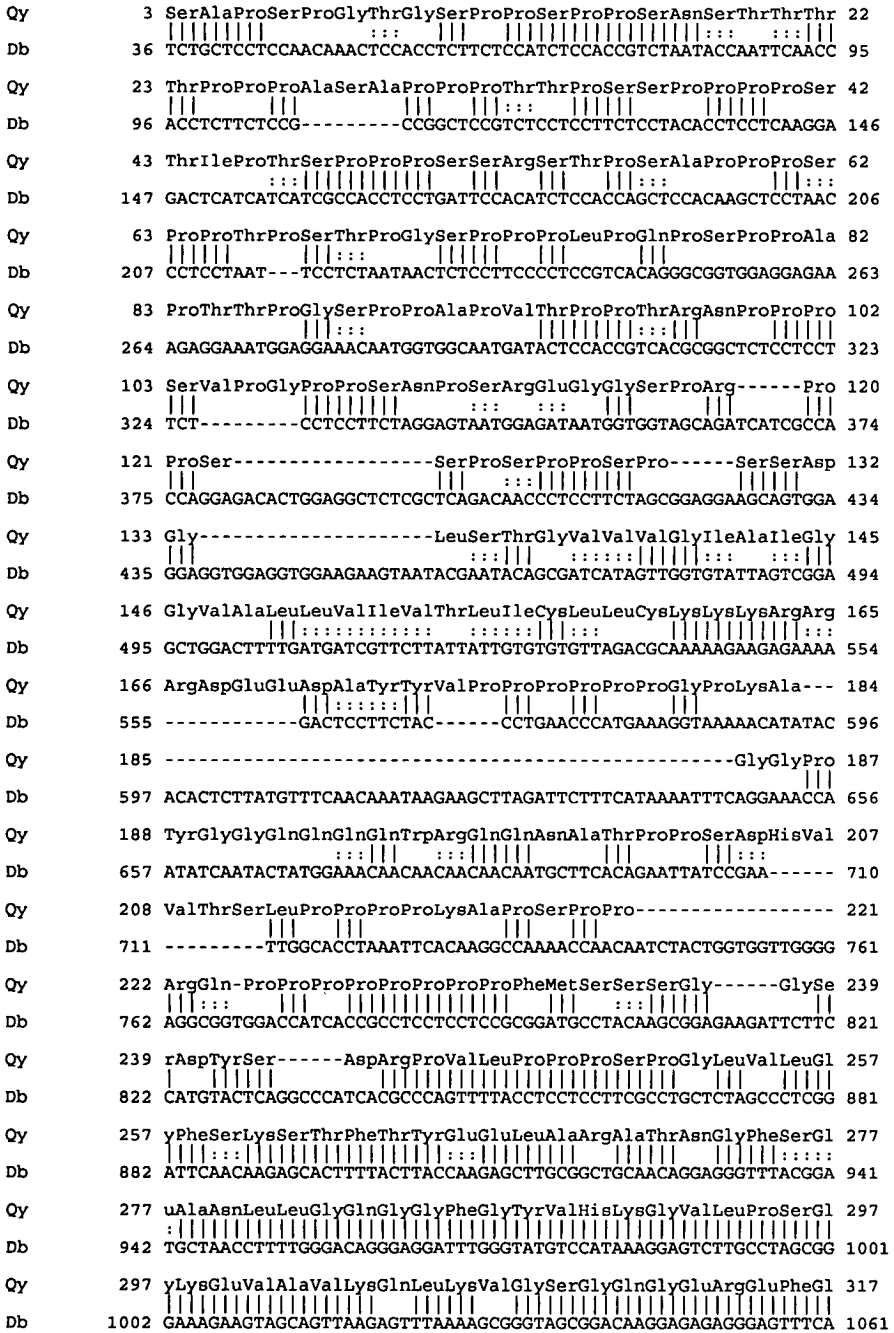


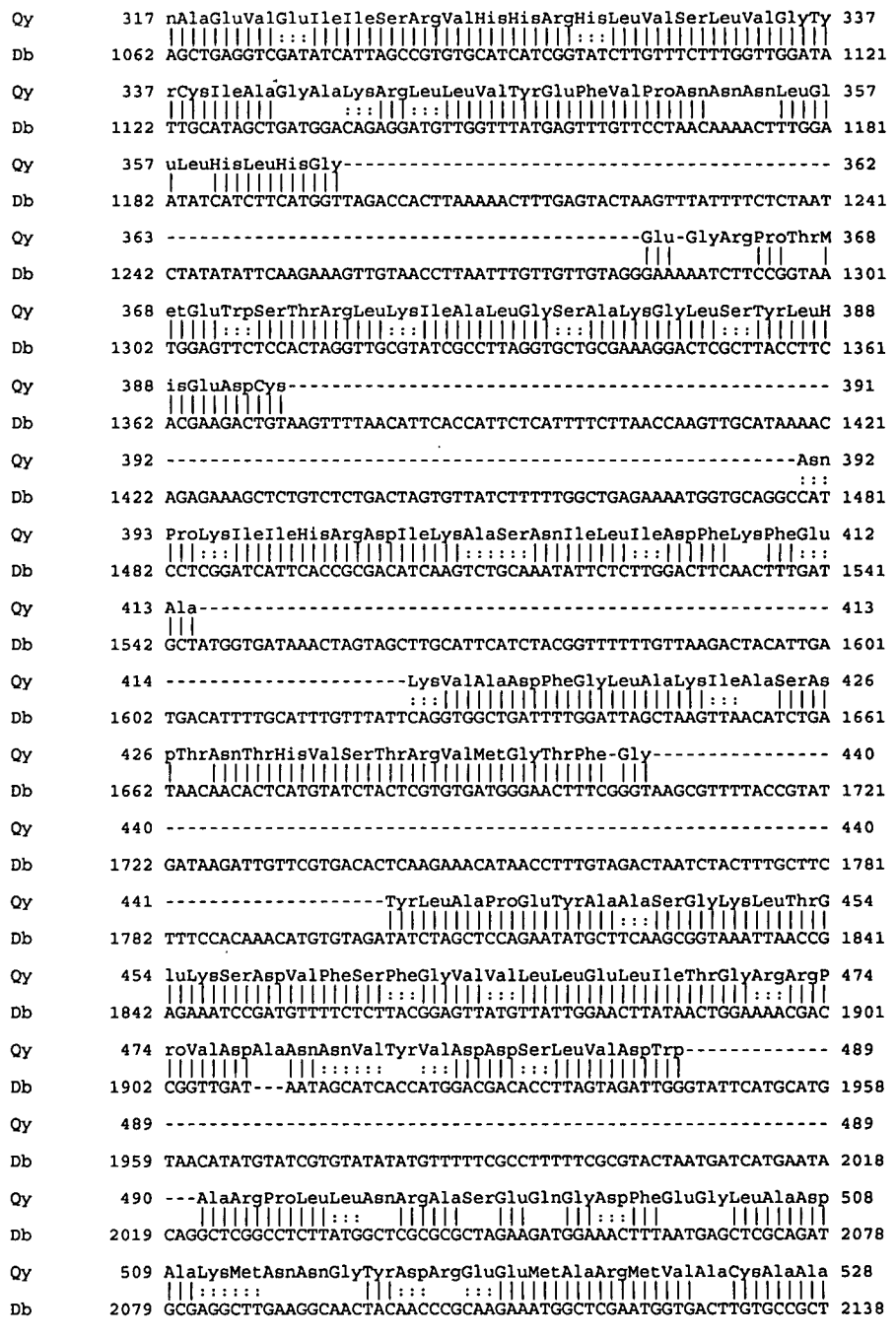
RESULT 10
ACF36551
ID ACF36551 standard; DNA; 2520 BP.
XX
AC ACF36551;
XX
DT 18-DEC-2003 (first entry)
XX
DE Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
DR P-PSDB; ABR82940.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 12; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents a PERK1 polypeptide related protein encoding genomic
CC DNA from A. thaliana (Accession NO. AAD15491)
XX
SQ Sequence 2520 BP; 717 A; 552 C; 538 G; 713 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.58e-36	Length:	2520
Score:	1504.00	Matches:	367
Percent Similarity:	53.47%	Conservative:	80
Best Local Similarity:	43.90%	Mismatches:	146
Query Match:	43.56%	Indels:	244
DB:	9	Gaps:	22

US-10-086-464-2 (1-647) x ACF36551 (1-2520)





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Db       2139 GCTAGCATTCGTCATTCGGGGCGTAAACGTCCAAAGATGAG-CCAGGTGAATCAAAATTA 2197

Qy        543 ----------------------------------------------------GlnIleVal 545

Db       2198 TAACTAAAAGTCTATTTTTGTCAGAGAATAACAAACAAATGTTGTGGTTTTCAGATAGTA 2257

Qy        546 ArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGln 565

Db       2258 AGAGCGTTAGAAGGAGAAGTGTCCTTAGATGCTTTAAACGAAGGTGTGAAGCCAGGACAC 2317

Qy        566 SerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGlu 585

Db       2318 AGTAACGTTTACGGGTCATTGGGAGCAAGCTCGGATTATAGTCAGACATCTTACAATGCA 2377

Qy        586 AspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr---------AsnAla 602

Db       2378 GACATGAAGAAATTCAGACAGATAGCTTTGTCGAGCCAAGAATTCCCAGTCAGTGACTGT 2437

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGly 614

Db       2438 GAAGGAACATCTAGTAATGATTCTAGAGATATGGGA 2473
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RESULT 11
AAF77097
ID AAF77097 standard; DNA; 2820 BP.
XX
AC AAF77097;
XX
DT 17-MAY-2001 (first entry)
XX
DE Arabidopsis gene #3.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,
PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Example; Fig 13; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 2820 BP; 819 A; 629 C; 577 G; 795 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2e-35	Length:	2820
Score:	1479.50	Matches:	367
Percent Similarity:	50.00%	Conservative:	99
Best Local Similarity:	39.38%	Mismatches:	151
Query Match:	42.85%	Indels:	318
DB:	4	Gaps:	28

US-10-086-464-2 (1-647) x AAF77097 (1-2820)

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Db         52 GTGGATTCATCTCCTGCCCCTGAAACC---TCAAATGGGACACCACCGTCAAACGGAACA 108

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40

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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60

Db        160 TCATCA---------ATATCTGCTCCTCCGCCAGATATCTCCGCTTCTTTTTCACCGCCG 210

Qy         61 ProSerProProThr---------------ProSerThrProGlySerProProProLeu 75

Db        211 CCTGCACCACCAACGCAAGAAACGTCACCTCCTACATCTCCGTCCTCATCGCCGCCTGTT 270

Qy         76 ---------------ProGln------------ProSerProProAlaPro------Thr 84

Db        271 GTAGCTAATCCGTCACCGCAGACTCCAGAGAATCCTTCTCCACCTGCACCTGAAGGCTCA 330

Qy         85 ThrProGlySerProProAla---ProValThrPro------------ProThrArgAsn 99

Db        331 ACTCCTGTAACGCCACCTGCACCACCACAAACACCGTCGAACCAATCACCGGAAAGACCA 390

Qy        100 ProProPro---------------------------------------------------- 102

Db        391 ACTCCTCCTTCTCCTGGTGCCAATGATGACCGAAACAGAACCAATGGCGGAAACAACAAC 450

Qy        103 ---------SerValProGlyProProSerAsnProSerArg---------GluGlyGly 116

Db        451 AGAGACGGCTCCACACCATCACCACCGTCGTCAGGGAACAGAACTTCCGGTGACGGTGGC 510

Qy        117 SerProArgProProSerSerProSerProProSerProSerSerAspGlyLeuSerThr 136

Db        511 TCACCTTCACCACCTCGGTCGATAAGCCCTCCTCAGAATAGTGGAGATTCAGACTCATCA 570

Qy        137 --------------------------GlyValValValGlyIleAlaIleGlyGlyVal 147

Db        571 TCGGGTAATCATCCACAAGCCAACATTGGATTGATTATTGGAGTCCTTGTAGGAGCAGGG 630

Qy        148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAsp 167

Db        631 CTTTTGCTTCTACTTGCAGTGTGTATTTGCATCTGTTGCAACAGGAAGAAGAAGAAGAAA 690

Qy        168 GluGluAspAla---------TyrTyrValProProProProProProGlyProLysAla 184

Db        691 TCTCCTCAGGTCAACCACATGCACTACTACAATAACAATCCTTATGGAGGAGCACCCTCA 750

Qy        185 Gly---------------------------------------------------------- 185

Db        751 GGTAATTACAGTTTAGTATAACTGGAATTTAATTTGTAGCCTAATGGTGTTTGATTAGGT 810

Qy        186 --------------------------------GlyProTyrGlyGlyGlnGlnGlnGln 194

Db        811 TTCAGAACGATCATAGTCTAATGGTTTCTGCTAGCTCCATATGGCAAAAGGATTAGATT- 869

Qy        195 TrpArgGlnGlnAsnAlaThr--------------------------------ProPro 203

Db        870 TATAAGCTAAAGGAGATGTTGCATAGTGTAGGTAATGGTGGTTATTACAAGGGAACACCT 929

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Db        930 CAAGATCATGTGGTG---AATATGGCTGGTCAAGGAGGTGGGAATTGGGGTCCACAGCAA 986

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
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Db        987 CCTGTGTCTGGTCCT-----------------CACAGTGATGCTTCCAACTTAACCGGT 1028

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Db       1029 CGAACTGCTATACCGTCACCTCAA---GCTGCAACTCTTGGTCACAACCAAAGCACTTTC 1085

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283

Db       1086 ACATACGATGAACTGTCCATTGCAACAGAAGGTTTCGCTCAGTCAAATTTGCTAGGACAA 1145

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303

Db       1146 GGAGGATTTGGGTATGTTCATAAAGGAGTTCTGCCTAGTGGCAAAGAAGTTGCAGTGAAG 1205

Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323

Db       1206 AGTCTTAAACTTGGAAGTGGACAAGGGGAACGCGAGTTTCAAGCAGAGGTTGATATCATT 1265

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343

Db       1266 AGCCGTGTCCATCATCGTCATCTCGTTTCTCTTGTTGGATATTGCATCTCTGGTGGTCAA 1325

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis------ 361

Db       1326 AGACTTTTGGTTTATGAGTTTATACCTAACAACACTCTTGAATTTCATCTTCATGGTACA 1385

Qy        361 ------------------------------------------------------------ 361

Db       1386 TTCATCTAACAGAATGTTTTCTTGTATTAACAAAACCTTTAAGTATGGTTTCTCTTTAAT 1445

Qy        362 ----------------------GlyGluGlyArgProThrMetGluTrpSerThrArgLe 374

Db       1446 CAGGAACATGATTGAAATTTCAGGAAAGGGTCGTCCGGTTTTGGATTGGCCTACAAGAGT 1505

Qy        374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys-------- 391

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Qy        391 ------------------------------------------------------------ 391

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Qy        392 ----------------------AsnProLysIleIleHisArgAspIleLysAlaSerAs 404

Db       1626 ATATGTTACATCAATTATAGGTCACCCTCGCATTATCCACAGAGATATCAAAGCTGCAAA 1685

Qy        404 nIleLeuIleAspPheLysPheGluAla------------------------------- 413

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Qy        413 ------------------------------------------------------------ 413

Db       1745 TACTTTTACTTTCATTGTCTCTCATTTTTGTTTCCAATCTGTGTCGATGTGTGTATCAGT 1804

Qy        414 ------------------LysValAlaAspPheGlyLeuAlaLysIleAlaSerAspTh 427

Db       1805 CTTATTGTGTAAATATATGCAGGTGGCAGATTTTGGATTGGCTAAGCTATCTCAAGACAA 1864

Qy        427 rAsnThrHisValSerThrArgValMetGlyThrPhe-Gly------------------- 440

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Qy        440 ------------------------------------------------------------ 440

Db       1925 CTCAACTCATCCACACTTATTTAGTTTCTTTCACTTGTTTTTAACATTTTCTTGGATTCA 1984

Qy        441 --TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheS 460

Db       1985 GATACTTAGCTCCAGAGTATGCATCAAGCGGAAAGTTATCCGACAAATCTGATGTTTTCT 2044

Qy        460 erPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnV 480

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Qy        480 alTyrValAspAspSerLeuValAspTrp------------------------------ 489

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Qy        489 ------------------------------------------------------------ 489

Db       2162 GTTTAATCCCAAAACACTTTCCAAAGCAAAAACAGAAACAAATCTTACTATTGTTGTTGC 2221

Qy        490 --AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspA 509

Db       2222 AGGCAAGGCCTTTGTGTTTGAAAGCAGCTCAAGATGGAGATTACAACCAATTGGCTGATC 2281

Qy        509 laLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaA 529

Db       2282 CACGTCTAGAGCTAAACTACAGTCATCAAGAGATGGTTCAAATGGCTTCTTGTGCAGCTG 2341

Qy        529 laCysValArgHisSerAlaArgArgArgProArgMetSerGlnIle------------- 544

Db       2342 CAGCAATCAGACATTCAGCAAGAAGACGGCCTAAGATGAGCCAGGT-TCAAAAACTCATA 2400

Qy        544 ------------------------------------------------------------ 544

Db       2401 CCACTTGTTGGTTCTATTGTTATATTTTTACTCACAATTAATCTTGATGATAAATGTGAC 2460

Qy        545 ----------------------------------------------ValArgAlaLeuGluG 550

Db       2461 ATACTAATGAATCTTGAAACATGTGTATGGTAAATGAAAAGATTGTACGAGCACTAGAAG 2520

Qy        550 lyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrS 570

Db       2521 GAGATATGTCAATGGATGATCTAAGTGAGGGAACAAGACCAGGACAAAGCACGTACTTGA 2580

Qy        570 erSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysP 590

Db       2581 GCCCCGGGAGCGTGAGCTCAGAGTATGACGCAAGCTCGTACACGGCAGACATGAAAAAGT 2640

Qy        590 heArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProT 610

Db       2641 TCAAGAAACTGGCGTTAGAGAATAAAGAATATCAAAGCAGT---GAATATGGTGGA---A 2694

Qy        610 hrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluM 630

Db       2695 CAAGTGAGTATGGCTTAAACCCTTCTGCTTCAAGTAGTGAA--------------GAAA 2739

Qy        630 etGluMetGlyLysIleLysArgThrGlyGln 640

Db       2740 TGAATAGAGGCTCAATGAAACGCAATCCTCAG 2771
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RESULT 12
ACF36552
ID ACF36552 standard; DNA; 2820 BP.
XX
AC ACF36552;
XX
DT 18-DEC-2003 (first entry)
XX
DE Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX

PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
DR P-PSDB; ABR82941.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 13; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents a PERK1 polypeptide related protein encoding genomic
CC DNA from A. thaliana (Accession NO. CAA18823)
XX
SQ Sequence 2820 BP; 819 A; 630 C; 576 G; 795 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.42e-35	Length:	2820
Score:	1471.50	Matches:	366
Percent Similarity:	49.89%	Conservative:	99
Best Local Similarity:	39.27%	Mismatches:	152
Query Match:	42.62%	Indels:	318
DB:	9	Gaps:	28

US-10-086-464-2 (1-647) x ACF36552 (1-2820)

```
Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
              :::   |||:::|||:::|||   |||   |||       :::||||||||||||   |||
Db         52 GTGGATTCATCTCCTGCCCCTGAAACC---TCAAATGGGACACCACCGTCAAACGGAACA 108

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
              :::         |||         :::   |||||||||   ||||||||||||||||||
Db        109 TCG---------CCGTCTAATGAGTCATCGCCGCCAACACCACCTTCTTCACCACCACCA 159

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
                 |||             |||   ||||||         |||         :::||||||
Db        160 TCATCA---------ATATCTGCTCCTCCGCCAGATATCTCCGCTTCTTTTTCACCGCCG 210

Qy         61 ProSerProProThr--------------ProSerThrProGlySerProProProLeu 75
              |||:::|||||||||              |||::::::|||   |||   ||||||:::
Db        211 CCTGCACCACCAACGCAAGAAACGTCACCTCCTACATCTCCGTCCTCATCGCCGCCTGTT 270

Qy         76 ---------------ProGln------------ProSerProProAlaPro------Thr 84
                           ||||||              ||||||||||||||||||      :::
Db        271 GTAGCTAATCCGTCACCGCAGACTCCAGAGAATCCTTCTCCACCTGCACCTGAAGGCTCA 330

Qy         85 ThrProGlySerProProAla---ProValThrPro------------ProThrArgAsn 99
              ||||||   :::|||||||||   |||   ||||||             |||   |||
Db        331 ACTCCTGTAACGCCACCTGCACCACCACAAACACCGTCGAACCAATCACCGGAAAGACCA 390

Qy        100 ProProPro---------------------------------------------------- 102
                 ||||||
Db        391 ACTCCTCCTTCTCCTGGTGCCAATGATGACCGAAACAGAACCAATGGCGGAAACAACAAC 450

Qy        103 ---------SerValProGlyProProSerAsnProSerArg---------GluGlyGly 116
                     |||   |||   |||||||||:::   :::|||          :::||||||
Db        451 AGAGACGGCTCCACACCATCACCACCGTCGTCAGGGAACAGAACTTCCGGTGACGGTGGC 510

Qy        117 SerProArgProProSerSerProSerProProSerProSerSerAspGlyLeuSerThr 136
              ||||||   ||||||   |||   |||||||||       |||   |||       |||:::
Db        511 TCACCTTCACCACCTCGGTCGATAAGCCCTCCTCAGAATAGTGGAGATTCAGACTCATCA 570

Qy        137 --------------------------GlyValValValGlyIleAlaIleGlyGlyVal 147
                                        |||:::::::::|||:::   :::|||
Db        571 TCGGGTAATCATCCACAAGCCAACATTGGATTGATTATTGGAGTCCTTGTAGGAGCAGGG 630

Qy        148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAsp 167
                 ||||||::::::       ||||||:::   |||   :::|||:::::::::
Db        631 CTTTTGCTTCTACTTGCAGTGTGTATTTGCATCTGTTGCAACAGGAAGAAGAAGAAGAAA 690

Qy        168 GluGluAspAla---------TyrTyrValProProProProProGlyProLysAla 184
                             :::|||           |||       |||       :::
Db        691 TCTCCTCAGGTCAACCACATGCACTACTACAATAACAATCCTTATGGAGGAGCACCCTCA 750

Qy        185 Gly---------------------------------------------------------- 185
              |||
Db        751 GGTAATTACAGTTTAGTATAACTGGAATTTAATTTGTAGCCTAATGGTGTTTGATTAGGT 810

Qy        186 --------------------------------GlyProTyrGlyGlyGlnGlnGlnGln 194
                                             |||||||||   :::   :::
Db        811 TTCAGAACGATCATAGTCTAATGGTTTCTGCTAGCTCCATATGGCAAAAGGATTAGATT- 869

Qy        195 TrpArgGlnGlnAsnAlaThr--------------------------------ProPro 203
              ::::::   :::                                        |||
Db        870 TATAAGCTAAAGGAGATGTTGCATAGTGTAGGTAATGGTGGTTATTACAAGGGAACACCT 929

Qy        204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223
                 ||||||||||||   ::::::                                |||:::|||
Db        930 CAAGATCATGTGGTG---AATATGGCTGGTCAAGGAGGTGGGAATTGGGGTCCACAGCAA 986

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
              |||         |||                 |||       |||:::   :::
Db        987 CCTGTGTCTGGTCCT-----------------CACAGTGATGCTTCCAACTTAACCGGT 1028

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
              |||       :::|||   |||                 ||||||   ::::::||||||||
Db       1029 CGAACTGCTATACCGTCACCTCAA---GCTGCAACTCTTGGTCACAACCAAAGCACTTTC 1085

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
              ||||||:::||||||:::   ||||||   ||||||:::::::::||||||||||||||||
Db       1086 ACATACGATGAACTGTCCATTGCAACAGAAGGTTTCGCTCAGTCAAATTTGCTAGGACAA 1145

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 GGAGGATTTGGGTATGTTCATAAAGGAGTTCTGCCTAGTGGCAAAGAAGTTGCAGTGAAG 1205

Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
              ||||||:::|||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1206 AGTCTTAAACTTGGAAGTGGACAAGGGGAACGCGAGTTTCAAGCAGAGGTTGATATCATT 1265

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
              ||||||||||||||||||||||||||||||||||||||||||||||||:::      :::
Db       1266 AGCCGTGTCCATCATCGTCATCTCGTTTCTCTTGTTGGATATTGCATCTCTCGTGGTCAA 1325

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis------ 361
              ||||||||||||||||||:::|||||||||   ||||||   |||||||||
Db       1326 AGACTTTTGGTTTATGAGTTTATACCTAACAACACTCTTGAATTTCATCTTCATGGTACA 1385

Qy        361 ---------------------------------------------------------- 361

Db       1386 TTCATCTAACAGAATGTTTTCTTGTATTAACAAAACCTTTAAGTATGGTTTCTCTTTAAT 1445

Qy        362 ----------------------GlyGluGlyArgProThrMetGluTrpSerThrArgLe 374
                                     |||:::|||||||||   ::::::|||   ||||||::
Db       1446 CAGGAACATGATTGAAATTTCAGGAAAGGGTCGTCCGGTTTTGGATTGGCCTACAAGAGT 1505

Qy        374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys-------- 391
              :|||||||||||||||||||:::||||||:::|||||||||||||||||
Db       1506 GAAGATTGCATTGGGATCAGCTAGAGGCCTTGCATATTTGCATGAAGACTGTAAGAAAAT 1565
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Qy       391 ------------------------------------------------------------ 391

Db      1566 CTTTATCTCACATATTTGCATCAGTTTCTATCTCGCTCTCTACAATATTTGAAAGATTGT 1625

Qy       392 ---------------------AsnProLysIleIleHisArgAspIleLysAlaSerAs 404
                                 :::|||:::|||||||||||||||||||||||||:::||
Db      1626 ATATGTTACATCAATTATAGGTCACCCTCGCATTATCCACAGAGATATCAAAGCTGCAAA 1685

Qy       404 nIleLeuIleAspPheLysPheGluAla------------------------------- 413
             |||||||:::||||||   ||||||
Db      1686 CATTCTTCTTGATTTCAGTTTTGAGAC-CAAGGTATGTGTGTATATATCGACTCTTGTAC 1744

Qy       413 ------------------------------------------------------------ 413

Db      1745 TACTTTTACTTTCATTGTCTCTCATTTTTGTTTCCAATCTGTGTCGATGTGTGTATCAGT 1804

Qy       414 ------------------LysValAlaAspPheGlyLeuAlaLysIleAlaSerAspTh 427
                              :::||||||||||||||||||||||||:::::::   |||
Db      1805 CTTATTGTGTAAATATATGCAGGTGGCAGATTTTGGATTGGCTAAGCTATCTCAAGACAA 1864

Qy       427 rAsnThrHisValSerThrArgValMetGlyThrPhe-Gly------------------- 440
             |||||||||||||||||||||||||||||||||||| |||
Db      1865 CTATACTCATGTCTCCACTCGCGTCATGGGAACTTTTGGGTAAGCAGCTTTGTAAAATGT 1924

Qy       440 ------------------------------------------------------------ 440

Db      1925 CTCAACTCATCCACACTTATTTAGTTTCTTTCACTTGTTTTTAACATTTTCTTGGATTCA 1984

Qy       441 --TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheS 460
               |||||||||||||||||||:::|||||||||||:::::::||||||||||||||||
Db      1985 GATACTTAGCTCCAGAGTATGCATCAAGCGGAAAGTTATCCGACAAATCTGATGTTTTCT 2044

Qy       460 erPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnV 480
             ||||||||||:::|||||||||||||||||||||||||   |||:::|||
Db      2045 CATTTGGAGTAATGCTTCTTGAGCTCATAACCGGAAGACCTCCTCTGGATCTAACTGGA- 2103

Qy       480 alTyrValAspAspSerLeuValAspTrp------------------------------ 489
                 ::::::||||||||||||||||||
Db      2104 --GAAATGGAAGATAGCTTGGTAGATTGGGTAAGTCGGTCCCCGCCTCTTCGGTTTACTT 2161

Qy       489 ------------------------------------------------------------ 489

Db      2162 GTTTAATCCCAAAACACTTTCCAAAGCAAAAACAGAAACAAATCTTACTATTGTTGTTGC 2221

Qy       490 --AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspA 509
               ||||||||||||      :::|||::::::   ||||||:::      |||||||||
Db      2222 AGGCAAGGCCTTTGTGTTTGAAAGCAGCTCAAGATGGAGATTACAACCAATTGGCTGATC 2281

Qy       509 laLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaA 529
               ::::::          |||      :::||||||   :::|||   :::||||||||||
Db      2282 CACGTCTAGAGCTAAACTACAGTCATCAAGAGATGGTTCAAATGGCTTCTTGTGCAGCTG 2341

Qy       529 laCysValArgHisSerAlaArgArgArgProArgMetSerGlnIle------------- 544
             ||   :::|||||||||||||||||||||||:::|||||||||
Db      2342 CAGCAATCAGACATTCAGCAAGAAGACGGCCTAAGATGAGCCAGGT-TCAAAAACTCATA 2400

Qy       544 ------------------------------------------------------------ 544

Db      2401 CCACTTGTTGGTTCTATTGTTATATTTTTACTCACAATTAATCTTGATGATAAATGTGAC 2460

Qy       545 ---------------------------------------------ValArgAlaLeuGluG 550
                                                         |||||||||||||||
Db      2461 ATACTAATGAATCTTGAAACATGTGTATGGTAAATGAAAAGATTGTACGAGCACTAGAAG 2520

Qy       550 lyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrS 570
             ||::::::|||:::   |||||||:::||||||   ||||||||||||||         |
Db      2521 GAGATATGTCAATGGATGATCTAAGTGAGGGAACAAGACCAGGACAAAGCACGTACTTGA 2580

Qy       570 erSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysP 590
             ||           |||::::::|||||:::|||   |||      ||||||||||||
Db      2581 GCCCCGGGAGCGTGAGCTCAGAGTATGACGCAAGCTCGTACACGGCAGACATGAAAAAGT 2640

Qy       590 heArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProT 610
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                ||:::|||:::||||||      :::||||||   ::::::   ||||||         |
Db      2641 TCAAGAAACTGGCGTTAGAGAATAAAGAATATCAAAGCAGT---GAATATGGTGGA---A 2694

Qy       610 hrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluM 630
             |||||:::|||||||||   ||||||   ||||||||||||               ||||
Db      2695 CAAGTGAGTATGGCTTAAACCCTTCTGCTTCAAGTAGTGAA--------------GAAA 2739

Qy       630 etGluMetGlyLysIleLysArgThrGlyGln 640
             ||      |||   :::||||||      |||
Db      2740 TGAATAGAGGCTCAATGAAACGCAATCCTCAG 2771

RESULT 13
AAF77095
ID   AAF77095 standard; DNA; 2880 BP.
XX
AC   AAF77095;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Arabidopsis gene #1.
XX
KW   Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200114563-A1.
XX
PD   01-MAR-2001.
XX
PF   18-AUG-2000; 2000WO-CA000966.
XX
PR   19-AUG-1999;   99US-0149466P.
PR   13-OCT-1999;   99US-0159122P.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
XX
PI   Goring D,  Silva N;
XX
DR   WPI; 2001-244305/25.
XX
PT   New proline-rich, extensin-like receptor kinase nucleic acids and
PT   polypeptides useful for increasing plant wounding or pathogen resistance,
PT   or for producing transgenic plants with increased wounding or pathogen
PT   resistance.
XX
PS   Example; Fig 11; 91pp; English.
XX
CC   The present invention relates to proline-rich extensin-like receptor
CC   kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC   increasing the resistance of plants to wounding and pathogens. These are
CC   also useful for producing transgenic plants with increased wounding and
CC   pathogen resistance compared with a wild type plant, as well as in assays
CC   for identifying and developing compounds to inhibit and/or enhance
CC   polypeptide function directly
XX
SQ   Sequence 2880 BP; 814 A; 693 C; 569 G; 804 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-27         Length:         2880
Score:                  1209.50         Matches:        325
Percent Similarity:     43.85%          Conservative:   92
Best Local Similarity:  34.17%          Mismatches:     160
Query Match:            35.03%          Indels:         376
DB:                     4               Gaps:           26

US-10-086-464-2 (1-647) x AAF77095 (1-2880)

Qy         2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThr 21
               :::|||||||      |||         |||||||||||||||||:::::::|||::::::
Db        98 AACTCAGCTCTTCCACCTGTTGATTCCTCTCCTCCTAGTCCACCAGCTGATTCATCATCA 157

Qy        22 Thr--------------------ThrProProProAlaSer------------------ 28
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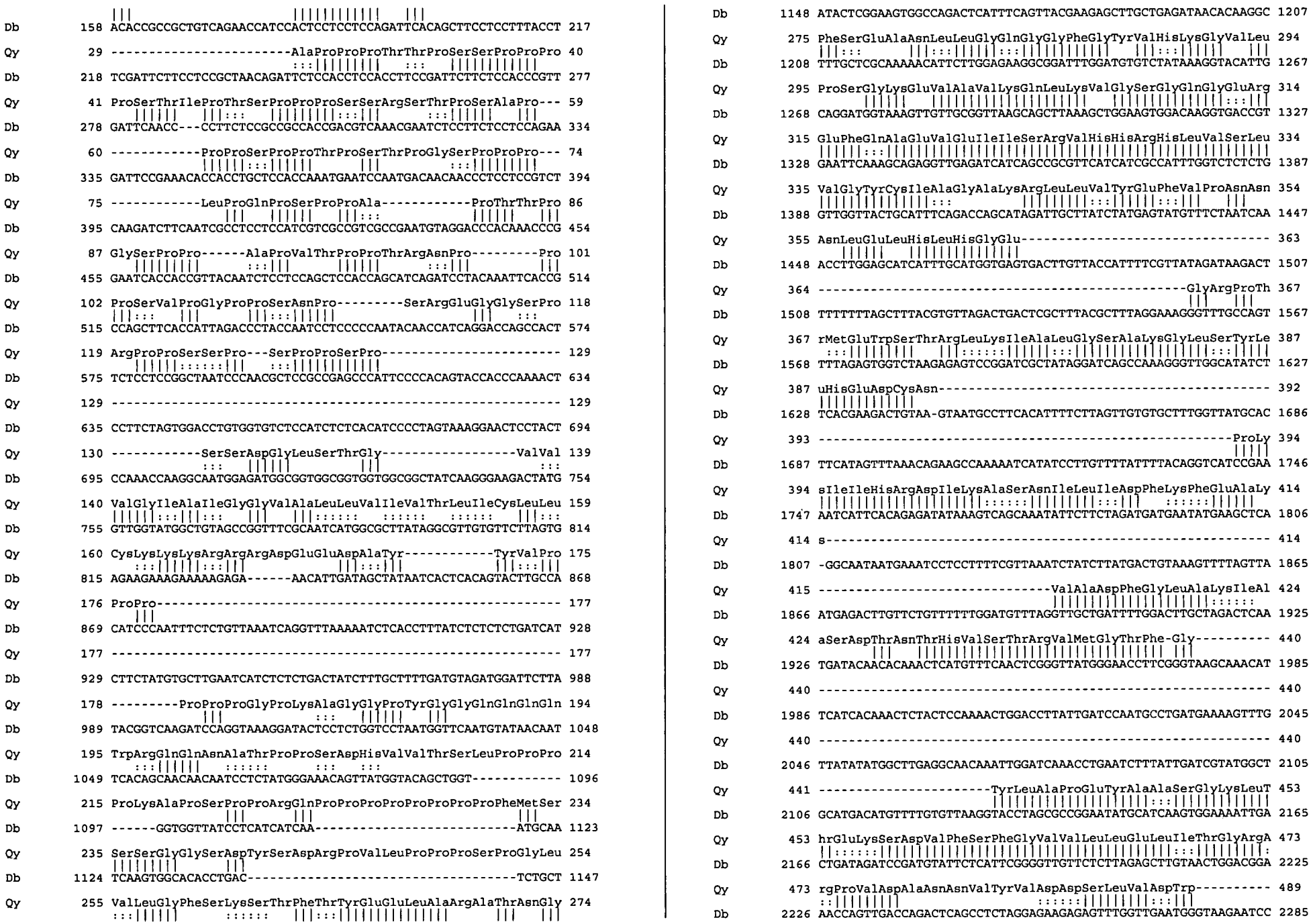

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Qy        489 ------------------------------------------------------------ 489

Db       2286 AACTTTCAAACATTCTTCAATAATAGTAAGATTGGCCCTAGTATACTTATATAGTACTTA 2345

Qy        490 --------------AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlu 504
                           ||||||||||||||   :::|||   |||   ||||||
Db       2346 TAAATGAACTCACAGGCGCGCCCGCTGCTTCTCAAAGCCATTGAGACCGGAGATTTAAGC 2405

Qy        505 GlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVal 524
              |||   |||   ::::::          |||          |||:::   ||||||:::
Db       2406 GAACTGATTGATACACGGCTTGAAAAGCGTTATGTGGAGCATGAAGTCTTCAGAATGATC 2465

Qy        525 AlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln--- 543
                 ||||||||||||||||||||||||||      :::||||||||||||   |||
Db       2466 GAGACAGCCGCTGCATGTGTTAGACATTCTGGTCCAAAACGCCCACGCATGGTTCAGGTA 2525

Qy        543 ------------------------------------------------------------ 543

Db       2526 ATTCTGACTAACCAAAAGTCCAAAGCTCCCATATATAGTAACAAGTGATTTCTCACATCT 2585

Qy        544 --------------------------IleValArgAlaLeuGluGlyAsnValSerLeu 554
                                       :::||||||||||||:::   :::
Db       2586 GAAAACTTATCTACTCTTCGAAATAAGGTTGTGAGAGCATTGGACTGCGACGGAGACTCG 2645

Qy        555 SerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGly 574
              |||::::::   |||::::::   ||||||
Db       2646 GGAGATATTAGCAACGGAATCAAAATTGGGCAA-------------------------- 2678

Qy        575 SerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAla 594
              ||||||   |||||||||   ||||||||||||||:::   ||||||||||||||||||
Db       2679 AGCACAACTTATGACTCAGGGCAATACAATGAAGACATTATGAAATTCAGGAAAATGGCG 2738

Qy        595 LeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
                 |||                  :::|||   ||||||                 |||
Db       2739 TTTGGTGGTGATAACAGCGTAGAGTCAGGATTGTACAGT-----------------GGA 2780

Qy        615 LeuTyrProSerGlySerSerSerGlu 623
                 |||   :::   |||||||||:::
Db       2781 AACTACTCTGCCAAAAGCTCTTCAGAT 2807

RESULT 14
ACF36550
ID   ACF36550 standard; DNA; 2880 BP.
XX
AC   ACF36550;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82939.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 11; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a PERK1 polypeptide related protein encoding genomic
CC   DNA from A. thaliana (Accession NO. AAC98010)
XX
SQ   Sequence 2880 BP; 814 A; 693 C; 569 G; 804 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-27       Length:          2880
Score:                  1209.50       Matches:         325
Percent Similarity:     43.85%        Conservative:    92
Best Local Similarity:  34.17%        Mismatches:      160
Query Match:            35.03%        Indels:          376
DB:                     9             Gaps:            26

US-10-086-464-2 (1-647) x ACF36550 (1-2880)

Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThr 21
              :::||||||      |||          |||||||||||||||||||:::::|||:::::
Db         98 AACTCAGCTCTTCCACCTGTTGATTCCTCTCCTCCTAGTCCACCAGCTGATTCATCATCA 157

Qy         22 Thr---------------------ThrProProProAlaSer------------------ 28
              |||                    ||||||||||||   |||
Db        158 ACACCGCCGCTGTCAGAACCATCCACTCCTCCTCCAGATTCACAGCTTCCTCCTTTACCT 217

Qy         29 ------------------------AlaProProProThrThrProSerSerProProPro 40
                                      :::|||||||||   :::   ||||||||||||
Db        218 TCGATTCTTCCTCCGCTAACAGATTCTCCACCTCCACCTTCCGATTCTTCTCCACCCGTT 277

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaPro--- 59
                 ||||||   |||:::   ||||||||:::|||      :::||||||   |||
Db        278 GATTCAACC---CCTTCTCCGCCGCCACCGACGTCAAACGAATCTCCTTCTCCTCCAGAA 334

Qy         60 ------------ProProSerProProThrProSerThrProGlySerProProPro--- 74
                        ||||||:::||||||      |||         :::||||||||||
Db        335 GATTCCGAAACACCACCTGCTCCACCAAATGAATCCAATGACAACAACCCTCCTCCGTCT 394

Qy         75 ------------LeuProGlnProSerProProAla------------ProThrThrPro 86
                           |||   ||||||   |||:::             ||||||   |||
Db        395 CAAGATCTTCAATCGCCTCCTCCATCGTCGCCGTCGCCGAATGTAGGACCCACAAACCCG 454

Qy         87 GlySerProPro------AlaProValThrProProThrArgAsnPro---------Pro 101
                 |||||||||      :::|||      ||||||      :::|||         |||
Db        455 GAATCACCACCGTTACAATCTCCTCCAGCTCCACCAGCATCAGATCCTACAAATTCACCG 514

Qy        102 ProSerValProGlyProProSerAsnPro---------SerArgGluGlyGlySerPro 118
              |||:::   |||      |||:::||||||                   |||   :::
Db        515 CCAGCTTCACCATTAGACCCTACCAATCCTCCCCCAATACAACCATCAGGACCAGCCACT 574

Qy        119 ArgProProSerSerPro---SerProProSerPro---------------------- 129
                 ||||||::::::|||   :::||||||||||||
Db        575 TCTCCTCCGGCTAATCCCAACGCTCCGCCGAGCCCATTCCCCACAGTACCACCCAAAACT 634

Qy        129 ------------------------------------------------------------ 129

Db        635 CCTTCTAGTGGACCTGTGGTGTCTCCATCTCTCACATCCCCTAGTAAAGGAACTCCTACT 694
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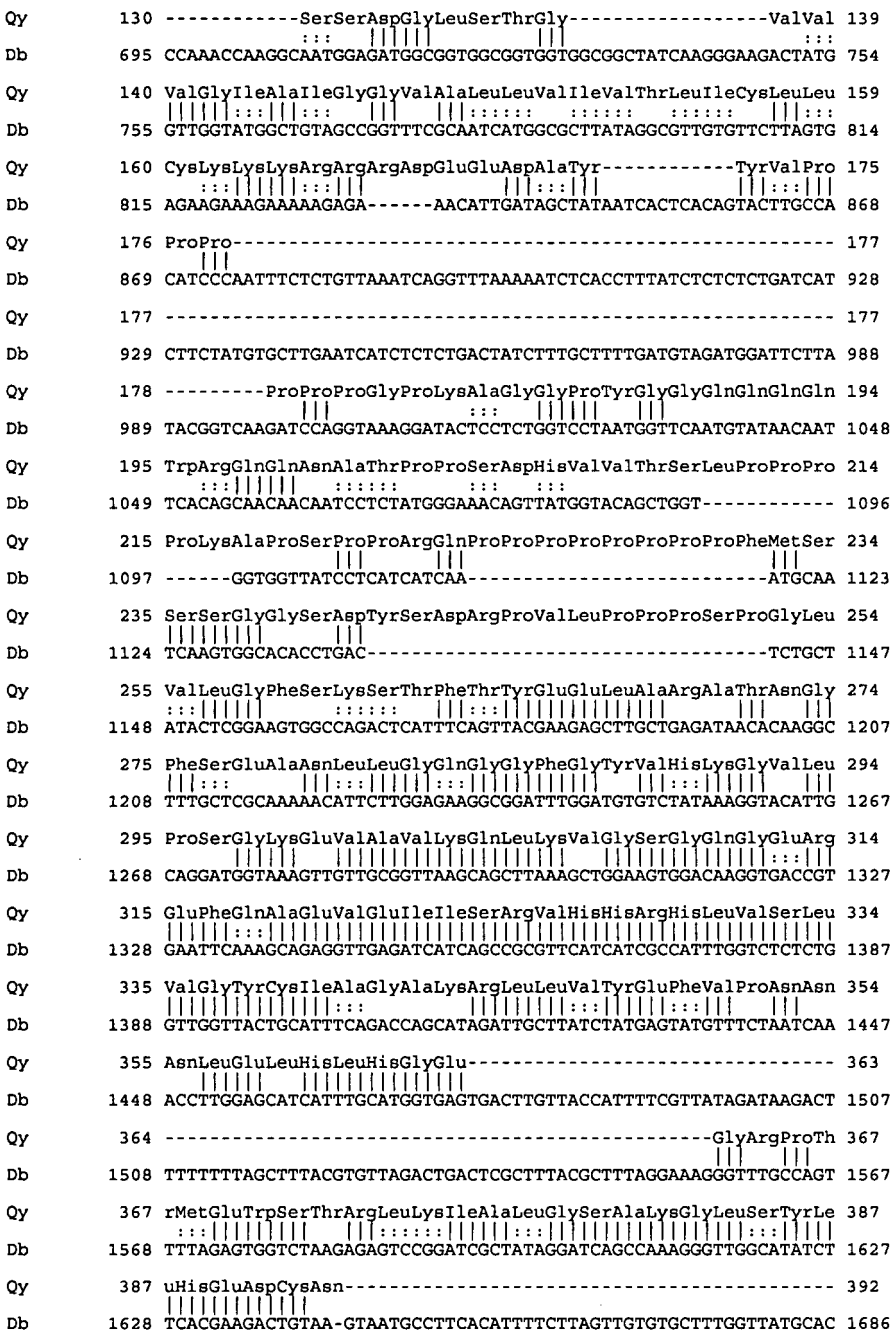

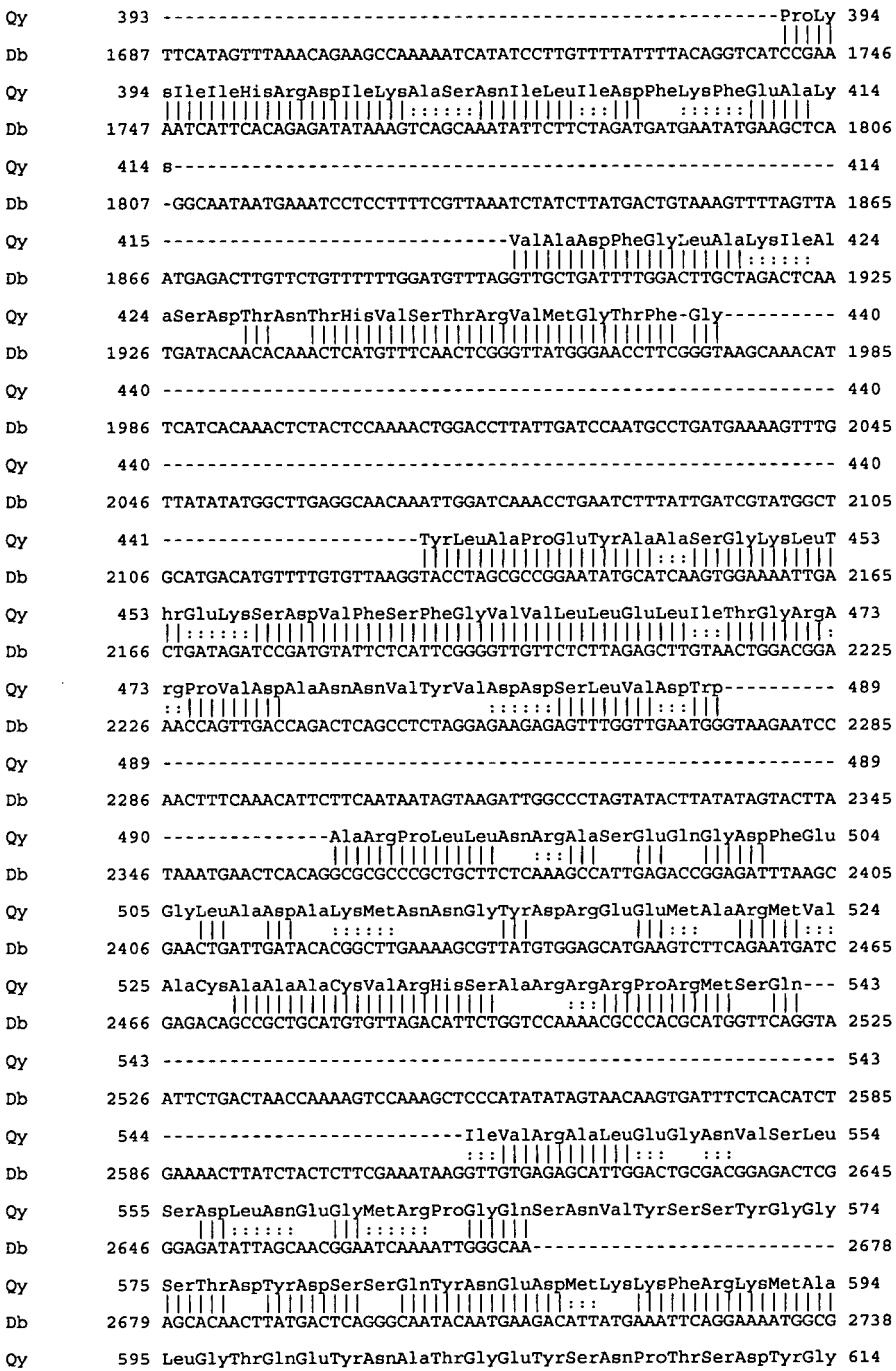

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                 |||                    :::|||   ||||||                  |||
Db       2739 TTTGGTGGTGATAACAGCGTAGAGTCAGGATTGTACAGT------------------GGA 2780

Qy        615 LeuTyrProSerGlySerSerSerGlu 623
                 |||   :::   |||||||||:::
Db       2781 AACTACTCTGCCAAAAGCTCTTCAGAT 2807

RESULT 15
ACF36553
ID   ACF36553 standard; DNA; 3060 BP.
XX
AC   ACF36553;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82942.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 14; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a PERK1 polypeptide related protein encoding genomic
CC   DNA from A. thaliana (Accession NO. CAA18590)
XX
SQ   Sequence 3060 BP; 797 A; 766 C; 592 G; 905 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.1e-27        Length:         3060
Score:                  1185.00        Matches:        342
Percent Similarity:     39.28%         Conservative:   72
Best Local Similarity:  32.45%         Mismatches:     185
Query Match:            34.32%         Indels:         456
DB:                     9              Gaps:           31

US-10-086-464-2 (1-647) x ACF36553 (1-3060)

Qy          2 SerSerAlaProSerProGlyThrGlySerProPro----------------------- 13
              ||||||:::|||:::|||   |||   |||||||||
Db         43 TCTTCCTCGCCGGCTCCGGCAACT---TCCCCGCCTGCCATGTCATTACCTCCGGCAGAT 99

Qy         14 -----------------SerProProSerAsnSerThrThrThrThrProProProAla 27
                               |||||||||:::           :::    |||||||||
Db        100 TCCGTACCTGACACGTCATCACCTCCAGCTCCTCCTTTGTCTCCTCTTCCCCCACCATTG 159

Qy         28 SerAlaProProProThrThrProSerSerProPro----------------------- 39
              |||:::|||||||||         ||||||   ||||||
Db        160 AGCTCTCCTCCGCCG---TTGCCTTCACCACCGCCTCTCTCCGCTCCCACCGCTTCCCCA 216

Qy         40 --------------------ProProSerThrIleProThrSerProProProSerSer 52
                                  |||||||||            |||||||||||
Db        217 CCGCCTCTTCCGGTTGAATCCCCACCGTCTCCTCCTATAGAATCACCACCGCCTCCTCTA 276

Qy         53 ArgSerThrProSerAlaProPro---------ProSerProProThrPro------Ser 67
                 :::|||      ||||||         ||||||||||||:::|||        |||
Db        277 CTGGAATCACCTCCTCCTCCTCCGTTGGAATCTCCATCTCCACCGTCTCCTCACGTCTCA 336

Qy         68 ThrProGlySerProProProLeuPro------------GlnProSerProProAlaPro 83
                 |||         ||||||||||||             :::||||||||||||
Db        337 GCTCCTTCCGGTTCACCGCCATTACCCTTCCTTCCCGCCAAACCTTCTCCGCCG------ 390

Qy         84 ThrThrProGlySerProProAlaProValThrProPro------ThrArgAsnProPro 101
                    |||   |||||||||:::         ||||||        |||   :::||||||
Db        391 ------CCTTCTTCACCTCCCTCCGAGACAGTTCCGCCGGGAAATACGATTTCTCCACCA 444

Qy        102 Pro-------------------------------------SerValProGlyProPro 108
              |||                                      :::   |||   ||||||
Db        445 CCTCGTTCACTTCCCTCCGAATCAACCCCGCCGGTGAACACAGCTTCTCCTCCACCGCCA 504

Qy        109 SerAsnProSerArgGluGlyGlySerProArgPro----------------------- 120
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Db        505 TCTCCTCCTCGCCGCCGTAGTGGC---CCTAAGCCTTCGTTTCCTCCTCCCATCAATTCT 561

Qy        121 ---ProSerSerProSerPro--------------------------------------- 126
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Db        562 TCTCCACCAAATCCTTCTCCGAACACTCCGTCACTCCCAGAAACTTCTCCTCCACCTAAA 621

Qy        127 -----------------ProSerProSerSer-------------------------- 131
                                |||   |||||||||
Db        622 CCACCGCTCTCAACGACGCCATTTCCCTCCTCATCCACTCCCCCGCCTAAGAAGTCCCCT 681

Qy        132 --------------------------------------------AspGlyLeu------ 134
                                                          ||||||
Db        682 GCAGCAGTAACTCTTCCTTTCTTTGGGCCAGCGGGCCAATTACCGGATGGGACCGTAGCA 741

Qy        134 ------------------------------------------------------------ 134

Db        742 CCTCCTATTGGGCCTGTTATAGAGCCCAAGACGAGTCCAGCCGAATCAATATCTCCGGGA 801

Qy        135 ---------------------------------------------------------Ser 135
                                                                       |||
Db        802 ACGCCACAGCCACTGGTTCCGAAGAGTCTACCTGTAACGACGTCGTATCACCGATCATCC 861

Qy        136 ThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeu 155
                 |||   :::   |||      |||   |||      ||||||:::::::::   |||
Db        862 GCCGGATTCTTATTTGGCGGTGTAATCGTTGGAGCTCTTCTACTAATTCTGTTAGGTCTT 921

Qy        156 IleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAsp-AlaTyrTyrValPr 175
              :::   :::      :::      |||   |||:::            |||      :::
Db        922 CTCTTTGTCTTCTACAGAGCTACCAGAAATAGAAATAACAACAGCAGCTCTGCTCATCAT 981

Qy        175 oProProProProPro------------------------------------------- 180
                 |||      |||
Db        982 CAATCCAAAACTCCCTCAAAAGGTATAAACTTTGAGATCAATTTGTTTCAGACTGTCACT 1041

Qy        181 -------------GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpAr 196
                              |||                     |||      |||      ||
Db       1042 TAAAATGTAATGTAATTGTAAGTTATGATCTTTTTTGCTTGGATCAGTTCAACATCATCG 1101

Qy        196 gGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProProProLy 216
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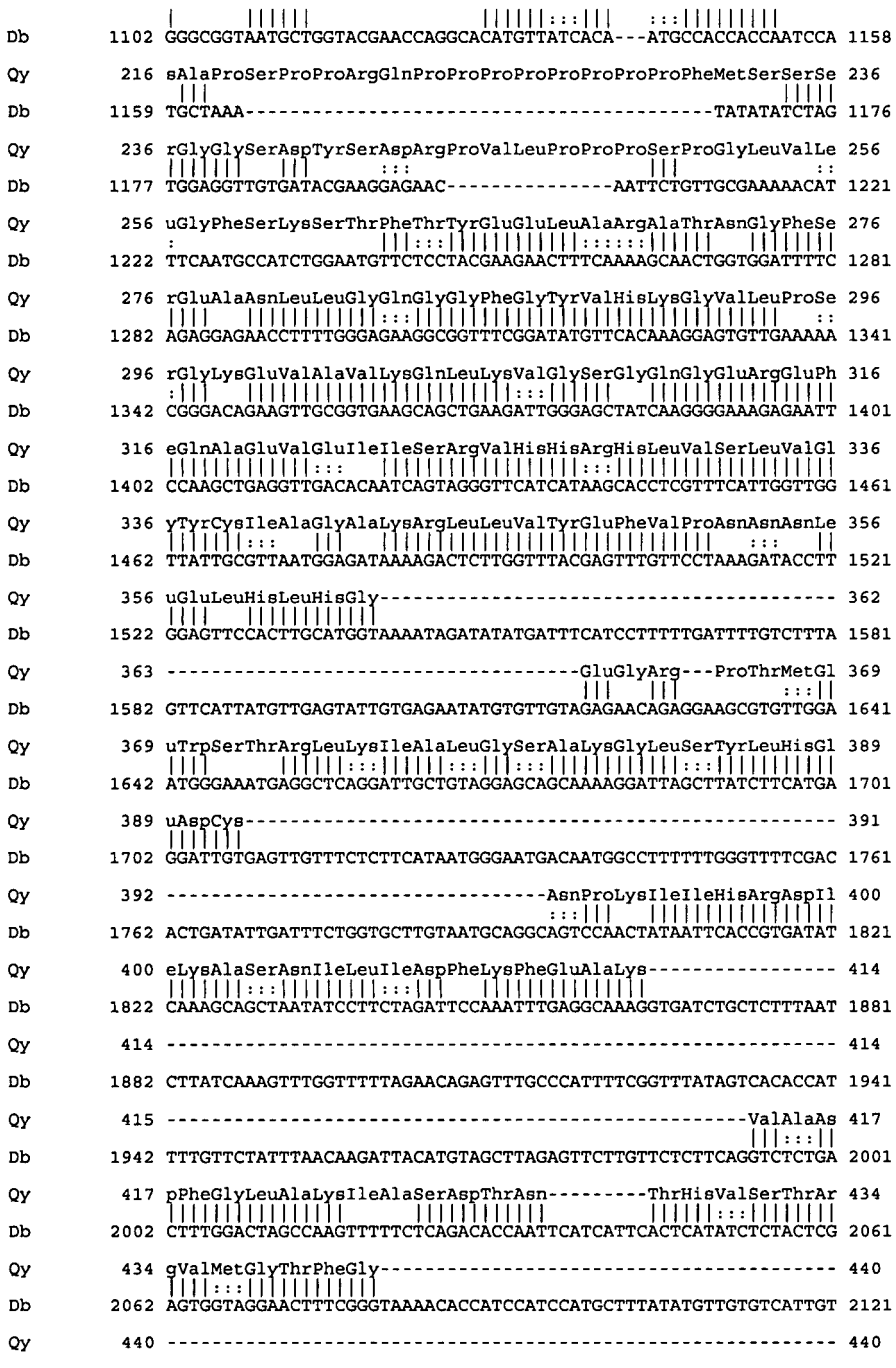

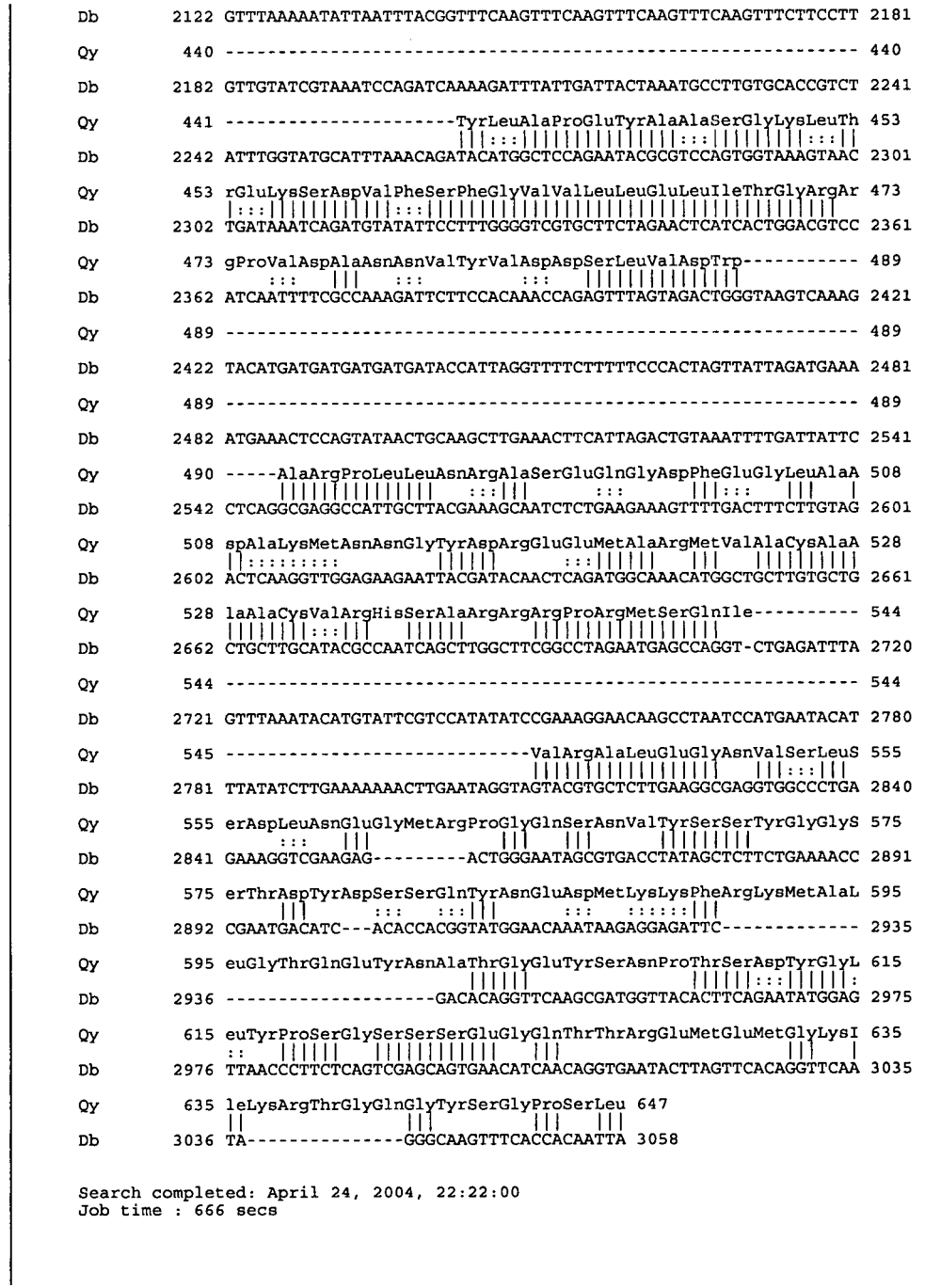

Search completed: April 24, 2004, 22:22:00
Job time : 666 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2004, 20:12:36 ; Search time 3601 Seconds
(without alignments)
5365.407 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10086464_@CGN_1_1_4237_@runat_23042004_083015_5625 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
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6: em_estpl:*
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8: em_htc:*
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12: gb_est3:*
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19: em_gss_pln:*
20: em_gss_vrt:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1092.5	31.6	1084	12	BP184771	BP184771 BP184771
2	1090.5	31.6	824	14	CD435142	CD435142 EL01N0355
3	1086	31.5	788	14	CF436437	CF436437 EST672782
4	1071	31.0	789	14	CF436655	CF436655 EST673000
5	1069	31.0	759	12	BM408099	BM408099 EST582426
6	1066	30.9	785	14	CF436122	CF436122 EST672467
7	1065	30.8	757	12	BG596561	BG596561 EST495239
8	1063	30.8	731	14	CB655196	CB655196 OSJNEc08F
9	1047	30.3	692	12	BG441204	BG441204 GA__Ea001
10	1030	29.8	723	14	CD839231	CD839231 RFO2.114I
11	1027.5	29.8	1053	11	AY108241	AY108241 Zea mays
12	1025	29.7	1016	11	AY108243	AY108243 Zea mays
13	1018	29.5	666	12	BM358715	BM358715 GA__Ea001
14	1013	29.3	695	13	CA072174	CA072174 SCCCAM100
15	983	28.5	715	13	BU099573	BU099573 WHE3309_A
16	961	27.8	770	13	BQ999193	BQ999193 QGG21G04.
17	931	27.0	611	14	CA237156	CA237156 SCMCFL500
c 18	931	27.0	859	29	CC725849	CC725849 OGGAB66TC
19	929.5	26.9	809	14	CA765135	CA765135 AF53-Rpf_
20	928	26.9	850	29	CC668754	CC668754 OGGAB66TM
c 21	923.5	26.7	769	14	CK283399	CK283399 EST746121
22	921	26.7	618	14	CA269355	CA269355 SCBGRT307
23	921	26.7	651	14	CF478389	CF478389 RTWW3_18_
24	920	26.6	673	14	CA164704	CA164704 SCSBRZ312
c 25	919.5	26.6	938	29	CG333846	CG333846 OG0GA30TV
c 26	917.5	26.6	949	29	CG436431	CG436431 OGVGH77TV
27	912	26.4	679	13	BQ404121	BQ404121 GA__Ed006
28	904.5	26.2	674	14	CA298046	CA298046 SCMCFL802
29	903	26.2	595	14	CF015663	CF015663 QBL8b11.x
30	903	26.2	637	13	BQ134241	BQ134241 1091014D0
31	903	26.2	645	13	BQ506869	BQ506869 EST614284
c 32	897.5	26.0	899	14	CK096498	CK096498 UB16CPE10
33	895.5	25.9	682	13	CA095337	CA095337 SCCCCL500
34	895	25.9	641	14	CA248316	CA248316 SCCCFL509
c 35	895	25.9	725	29	CG450877	CG450877 OG7AK95TH
c 36	893.5	25.9	803	14	CF243440	CF243440 3530_1_21
37	891	25.8	646	13	BQ240617	BQ240617 TaE05015B
38	891	25.8	652	13	BQ849683	BQ849683 QGB10I20.
39	891	25.8	666	13	BU499754	BU499754 946178G10
40	891	25.8	691	14	CA237152	CA237152 SCMCFL500
41	889	25.7	626	13	BQ582873	BQ582873 E012278-0
42	888.5	25.7	593	10	BF176907	BF176907 EM1_4_B10
43	887	25.7	622	14	CA999610	CA999610 S345P_H09
44	887	25.7	673	13	BQ410602	BQ410602 GA__Ed003
45	886.5	25.7	573	9	AV551753	AV551753 AV551753

ALIGNMENTS

RESULT 1
BP184771
LOCUS BP184771 1084 bp mRNA linear EST 17-JUL-2003
DEFINITION BP184771 pNS rice panicle cDNA, germ cell generating stage Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.
ACCESSION BP184771
VERSION BP184771.1 GI:32948199
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

```
REFERENCE   1  (bases 1 to 1084)
  AUTHORS   Moriguchi,K., Ito,Y., Yamazaki,Y. and Kurata,N.
  TITLE     Finding of various plant nuclear proteins using yeast nuclear
            transportation trap system - a proteomal approach
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Kazuki Moriguchi
            Plant Genetics
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-55-981-6872
            Fax: 81-55-981-6879
            Email: kmoriguc@lab.nig.ac.jp
            cDNA clone obtained from nuclear transportation trap system
            encoding a protein similar to Oryza sativa (japonica
            cultivar-group) putative receptor protein kinase PERK1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:39947"
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                     /dev_stage="germ cell generating stage"
                     /clone_lib="pNS rice panicle cDNA, germ cell generating
                     stage"
ORIGIN

Alignment Scores:
Pred. No.:              4.98e-26        Length:         1084
Score:                  1092.50         Matches:        212
Percent Similarity:     82.88%          Conservative:   30
Best Local Similarity:  72.60%          Mismatches:     43
Query Match:            31.64%          Indels:         7
DB:                     12              Gaps:           3

US-10-086-464-2 (1-647) x BP184771 (1-1084)

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
              |||||||||:::||||||||||||||||||||    ||||||||||||||||||||||
Db          2 TTGCACGGAAAAGGCCGACCAACAATGGAGTGGCCCACAAGACTAAAGATTGCTTTGGGA 61

Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
              :::|||||||||||:::||||||||||||||||:::|||||||||||||||||||||||
Db         62 GCTGCAAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCTAAGATCATCCATCGTGAT 121

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419
              |||||||||||||||||||:::||||||||||||||:::|||||||||||||||||||
Db        122 ATTAAGGCGTCAAACATTCTTCTTGATTTTAAGTTTGAATCTAAGGTTGCTGATTTTGGA 181

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              ||||||||      ||||||    ||||||||||||||||||||||||||||||||||||
Db        182 CTTGCTAAGTTCACCAGTGATAATAACACTCATGTTTCGACAAGAGTAATGGGCACTTTT 241

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
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Db        242 GGATATCTAGCACCAGAGTACGCATCTTCTGGCAAGCTCACTGAGAAATCAGATGTCTTC 301

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
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Db        302 TCCTATGGAGTTATGCTTCTTGAGTTAATAACTGGTCGTCGGCCAGTTGATACAAGTCAA 361

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
              |||:::|||||||||||||||||||||||||||||||||||||   :::|||   |||
Db        362 ACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCTTTACTGATGCAAGCACTTGAG 421

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
              |||::::::|||   |||   |||   ::::::        ::::::      |||
Db        422 AATGGTAACTACGAGGAGTTAGTAGATCCTCGGCTTGGGAAGGATTTCAATCCCAATGAG 481

Qy        520 MetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPro 539
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        482 ATGGCGAGAATGATTGCTTGTGCAGCTGCATGCGTACGCCATTCCGCTCGTCGTCGCCCA 541

Qy        540 ArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGlu 559
              ||||||||||:::||||||||||||||||||||||:::|||||||||   ||||||||||
Db        542 CGCATGAGCCAGGTTGTCCGGGCTTTGGAAGGTGACGTGTCTTTGGAGGATCTTAATGAA 601

Qy        560 GlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAsp 579
              |||:::|||||||||   |||       :::   ||||||      |||:::|||||||||
Db        602 GGTGTTCGGCCTGGTCACAGCCGCTATTTTGGATCGTAC---AGCAGCTCTGACTATGAT 658

Qy        580 SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGlu 599
              |||   ||||||||||||||||||||||||||||||||||||||||      |||
Db        659 TCTGGCCAATACAACGAGGACATGAAGAAGTTCAGGAAGATGGCTTTT---ACCAACAAT 715

Qy        600 TyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGly 619
                 :::   :::   :::||||||   |||||||||:::||||||      ||||||
Db        716 AATGATACGAGCAGTCAATACAGCGCACCAACCAGCGAGTATGGCCAGATACCCTCTGCA 775

Qy        620 SerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly 639
              ||||||||||||||||||   |||:::|||:::|||            ||||||   |||
Db        776 TCAAGCAGCGAGGGCCAACAAACCCAGGAAGTCGAGAGCAGGACAACCAAGAGAGGCGGC 835

Qy        640 --------------GlnGlyTyrSerGlyProSer 646
                           ||||||||||||   |||
Db        836 TACAGTGGCTACAGCTCAGGATACAGCGGAGCCTCA 871

RESULT 2
CD435142
LOCUS       CD435142                824 bp    mRNA    linear   EST 03-JUN-2003
DEFINITION  EL01N0355D03.b Endosperm_3 Zea mays cDNA, mRNA sequence.
ACCESSION   CD435142
VERSION     CD435142.1  GI:31350785
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 824)
  AUTHORS   Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
            Messing,J.
  TITLE     Sequencing of the maize endosperm ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Lai, Jinsheng
            Dr. Joachim Messing's lab
            Waksman Institute, Rutgers University
            190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
            Tel: 732-445-3801
            Fax: 732-445-5735
            Email: jlai@waksman.rutgers.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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ORIGIN

Alignment Scores:
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Percent Similarity:     84.12%          Conservative:   27
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Query Match:            31.58%          Indels:         3
DB:                     14              Gaps:           2

US-10-086-464-2 (1-647) x CD435142 (1-824)

Qy        334 LeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsn 353
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RESULT 3
CF436437
LOCUS CF436437 788 bp mRNA linear EST 04-SEP-2003
DEFINITION EST672782 normalized cDNA library of onion Allium cepa cDNA clone ACACM44, mRNA sequence.
ACCESSION CF436437
VERSION CF436437.1 GI:34459127
KEYWORDS EST.
SOURCE Allium cepa (onion)
ORGANISM Allium cepa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
REFERENCE 1 (bases 1 to 788)
AUTHORS Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
TITLE Expressed Sequence Tags from a normalized library of mixed onion tissues (Allium cepa)
JOURNAL Unpublished (2003)
COMMENT Contact: Havey MJ
Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA
Tel: 608-262-1830
Fax: 608-262-4743
Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACACM44TR. For more information:
http://haveylab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Red Creole(bulbs), unknown(callus), Ebano & Texas Legend(roots)"
/db_xref="taxon:4679"
/clone="ACACM44"
/tissue_type="Callus, roots, and young bulbs"
/clone_lib="normalized cDNA library of onion"
/note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1: EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA from callus, roots, and young bulbs were combined to synthesize the library. Normalization to enrich for low-copy transcripts was performed by proprietary techniques of Invitrogen."
ORIGIN

Alignment Scores:

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Score:	1086.00	Matches:	204
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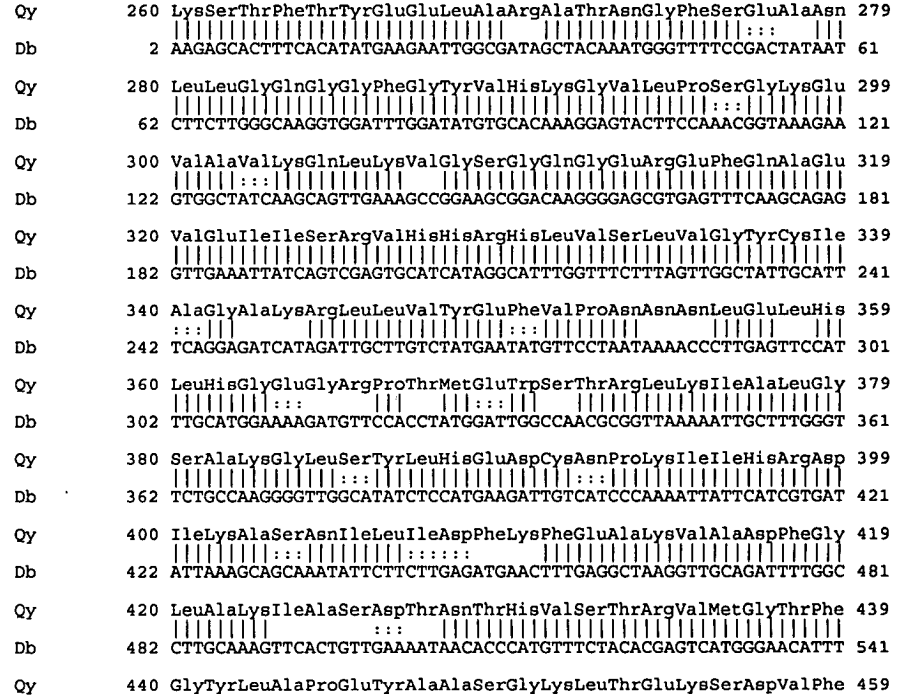
US-10-086-464-2 (1-647) x CF436437 (1-788)



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Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
Db        662 ACTTATACAGATGATAGTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGAG 721

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
Db        722 CATGATGATTATGATGAGCTCATTGACAGAAGGCTAGGAGATAAATACAACCATGACGAA 781

Qy        520 MetAla 521
Db        782 ATGGCA 787

RESULT 4
CF436655
LOCUS       CF436655                789 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST673000 normalized cDNA library of onion Allium cepa cDNA clone
            ACACK26, mRNA sequence.
ACCESSION   CF436655
VERSION     CF436655.1  GI:34459345
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACACK26TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .789
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACACK26"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

Alignment Scores:
Pred. No.:              1.82e-25        Length:         789
Score:                  1071.00         Matches:        203
Percent Similarity:     86.64%          Conservative:   24
Best Local Similarity:  77.48%          Mismatches:     35
Query Match:            31.02%          Indels:         0
DB:                     14              Gaps:           0
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US-10-086-464-2 (1-647) x CF436655 (1-789)

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
Db          2 AAGAGCACTTTCACATATGAAGAATTGGCGATAGCTACAAATGGGTTTTCCGACTATAAT 61

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGlu 299
Db         62 CTTCTTGGGCAAGGTGGATTTGGATATGTGCACAAAGGAGTACTTCCAAACGGTAAAGAA 121

Qy        300 ValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGlu 319
Db        122 GTGGCTATCAAGCAGTTGAAAGCCGGAAGCGGACAAGGGGAGCGTGAGTTTCAAGCAGAG 181

Qy        320 ValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIle 339
Db        182 GTTGAAATTATCAGTCGAGTGCATCATAGGCATTTGGTTTCTTTAGTTGGCTATTGCATT 241

Qy        340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHis 359
Db        242 TCAGGAGATCATAGATTGCTTGTCTATGAATATGTTCCTAATAAAACCCTTGAGTTCCAT 301

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
Db        302 TTGCATGGAAAAGATGTTCCACCTATGGATTGGCCAACGCGGTTAAAAATTGCTTTGGGT 361

Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
Db        362 TCTGCCAAGGGGTTGGCATATCTCCATGAAGATTGTCATCCCAAAATTATTCATCGTGAT 421

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419
Db        422 ATTAAAGCAGCAAATATTCTTCTTGAGATGAACTTTGAGGCTAAGGTTGCAGATTTTGGC 481

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
Db        482 CTTGCAAAGTTCACTGTTGAAAATAACACCCATGTTTCTACACGAGTCATGGGAACATTT 541

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
Db        542 GGGTATCTGGCACCAGAATATGCATCCTCTGGTAAACTAAGTGATAAATCAGATGTCTTT 601

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
Db        662 ACTTATACAGATGATAGTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGAG 721

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
Db        722 CATGATGATTATGATGAGCTCATTGACAGAAGGCTAGGAGATAAATACCACCCATGACGA 781

Qy        520 MetAla 521
Db        782 ATGGCA 787

RESULT 5
BM408099
LOCUS       BM408099                759 bp    mRNA    linear   EST 10-MAR-2003
DEFINITION  EST582426 potato roots Solanum tuberosum cDNA clone cPRO33O21 5'
            end, mRNA sequence.
ACCESSION   BM408099
VERSION     BM408099.1  GI:18259729
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
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            Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
            Tanksley,S. and Baker,B.
  TITLE     Generation of ESTs from potato roots
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cPRO33O21"
                     /tissue_type="roots"
                     /dev_stage="in vitro grown stem cuttings"
                     /lab_host="SOLR"
                     /clone_lib="potato roots"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Cornell University, Tanksley lab;
                     sequencing; The Institute for Genomic Research. Roots were
                     isolated from in vitro grown stem cuttings on CM medium.
                     Roots were isolated two weeks after placing the stem
                     cuttings from in vitro grown plants on medium."
ORIGIN

Alignment Scores:
Pred. No.:                2.04e-25      Length:          759
Score:                    1069.00       Matches:         200
Percent Similarity:       89.29%        Conservative:    25
Best Local Similarity:    79.37%        Mismatches:      27
Query Match:              30.96%        Indels:          0
DB:                       12            Gaps:            0

US-10-086-464-2 (1-647) x BM408099 (1-759)

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db          2 GGGGAACGTGAATTTCAGGCGGAAGTTGAGATTATTAGCCGAGTACATCACAAGCATCTT 61

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351
              ||||||||||||||||||||||||   |||||||:::|||||||||||||||||||||||
Db         62 GTGTCTCTTGTTGGATACTGCATTACTGGGGCTCAGAGACTGCTTGTTTATGAGTTTGTT 121

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371
              |||||||||   ||||||   ||||||||||||:::|||||||||   ::::::|||
Db        122 CCAAACAATACTTTGGAATTTCATTTACACGGAAAGGGAAGGCCTCCTTTGGATTGGCCA 181

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        182 ATACGGCTAAAGATTGCTCTAGGGTCAGCTAAAGGACTGGCATATCTGCATGAAGACTGC 241

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411
              |||||||||||||||||||||||||||:::|||||||||||||||||   |||
Db        242 CAACCGAAAATCATTCACCGTGATATCAAGGCAGCTAATATACTTATCGACTTTAATTTT 301

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisVal 431
              |||||||||||||||||||||||||||||:::   ||||||   ||||||||||||
Db        302 GAGGCTAAGGTTGCTGATTTTGGACTTGCCAAGCTAACTTCTGATGTTAATACTCATGTC 361

Qy        432 SerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLys 451
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db        362 TCCACCAGAGTGATGGGAACCTTTGGGTATTTGGCTCCAGAATATGCTTCCTCTGGAAAG 421

Qy        452 LeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGly 471
              ||||||:::|||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        422 CTTACAGACAAGTCAGACGTATTCTCCTTTGGTGTAATGCTTCTTGAGTTGATAACTGGA 481

Qy        472 ArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArg 491
              ||||||||||||||||:::         |||:::::|||||||||||||||||||||||||
Db        482 CGTCGGCCTGTTGACTCTACTCAATCATACATCGAAGATAGTTTGGTGGACTGGGCACGT 541

Qy        492 ProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMet 511
              |||||||||   ||||||   |||          |||:::   |||   |||   ::::::
Db        542 CCATTACTCACACGAGCTTTAGAAGATGAAAAGTTTGATACCCTTGTTGATCGTCGGCTA 601

Qy        512 AsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVal 531
                |||   |||:::      |||||||||||||||||||||||   ||||||||||||
Db        602 GAAAATGATTATAACCATAATGAGATGGCTCGCATGGTTGCTTGTTGTGCTGCTTGTGTG 661

Qy        532 ArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsn 551
              ||||||||||||:::|||||||||||||||:::|||:::::|||||||||||||||:::
Db        662 CGTCATTCAGCAAAGCGTAGACCACGAATGACACAGGTTCTCCGAGCCTTGGAAGGAGAT 721

Qy        552 ValSerLeuSerAspLeuAsnGluGlyMetArgPro 563
              |||||||||||||||||   ||||||::::::|||
Db        722 GTCTCATTATCAGACCTTTACGAAGGGATTAAACCT 757

RESULT 6
CF436122
LOCUS       CF436122                785 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST672467 normalized cDNA library of onion Allium cepa cDNA clone
            ACACJ26, mRNA sequence.
ACCESSION   CF436122
VERSION     CF436122.1  GI:34458812
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACACJ26TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACACJ26"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

Alignment Scores:
Pred. No.:                2.61e-25      Length:          785
Score:                    1066.00       Matches:         204
Percent Similarity:       86.64%        Conservative:    23
Best Local Similarity:    77.86%        Mismatches:      34
Query Match:              30.87%        Indels:          1
DB:                       14            Gaps:            0
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```
US-10-086-464-2 (1-647) x CF436122 (1-785)

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
              ||||||||||||||||||||||||||||||   ||||||||||||||||||:::   |||
Db          2 AAGAGCACTTTCACATATGAAGAATTGGCGATAGCTACAAATGGGTTTTCCGACTATAAT 61

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGlu 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db         62 CTTCTTGGGCAAGGTGGATTTGGATATGTGCACAAAGGAGTACTTCCAAACGGTAAAGAA 121

Qy        300 ValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGlu 319
              ||||||:::|||||||||||   ||||||||||||||||||||||||||||||||||||
Db        122 GTGGCTATCAAGCAGTTGAAAGCCGGAAGCGGACAAGGGGAGCGTGAGTTTCAAGCAGAG 181

Qy        320 ValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIle 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTTGAAATTATCAGTCGAGTGCATCATAGGCATTTGGTTTCTTTAGTTGGCTATTGCATT 241

Qy        340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHis 359
              :::|||      |||||||||||||||||:::|||||||||      ||||||   |||
Db        242 TCAGGAGATCATAGATTGCTTGTCTATGAATATGTTCCTAATAAAACCCTTGAGTTCCAT 301

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
              |||||||||::      |||   |||:::|||   ||||||||||||||||||||||
Db        302 TTGCATGGAAAAGATGTTCCACCTATGGATTGGCCAACGCGGTTAAAAATTGCTTTGGGT 361

Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
              ||||||||||||||:::||||||||||||||||||:::||||||||||||||||||||||
Db        362 TCTGCCAAGGGGTTGGCATATCTCCATGAAGATTGTCATCCCAAAATTATTCATCGTGAT 421

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419
              |||||||||:::|||||||||::::::      ||||||||||||||||||||||||||
Db        422 ATTAAAGCAGCAAATATTCTTCTTGAGATGAACTTTGAGGCTAAGGTTGCAGATTTTGGC 481

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              |||||||||         :::   ||||||||||||||||||||||||||||||||||
Db        482 CTTGCAAAGTTCACTGTTGAAAATAACACCCATGTTTCTACACGAGTCATGGGAACATTT 541

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
              ||||||||||||||||||||||:::||||||||||::::::||||||||||||||||||
Db        542 GGGTATCTGGCACCAGAATATGCATCCTCTGGTAAACTAAGTGATAAATCAGATGTCTTT 601

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
              ||||||||||||:::|||||||||||||||||||:::||||||||||||||||||||||
Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSer-LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGl 499
              |||   |||||||||| ||||||||||||||||||||||||   :::|||   ||
Db        662 ACTTATACAGATGATAGTTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGA 721

Qy        499 uGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGl 519
              |     |||::::::   |||   |||   |||          |||:::   :::||
Db        722 GCATGATGATTATGATGAGCTCATTGACAGAAAGGCTAGGAGATAATACAACCATGACGA 781

Qy        519 uMet 520
              ||||
Db        782 AATG 785

RESULT 7
BG596561
LOCUS       BG596561               757 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST495239 cSTS Solanum tuberosum cDNA clone cSTS15A23 5' sequence,
            mRNA sequence.
ACCESSION   BG596561
VERSION     BG596561.1  GI:13614701
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from sprouting potato eyes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTS15A23"
                     /tissue_type="sprouting eyes from tubers"
                     /dev_stage="12-14 weeks post harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTS"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
                     taken from tubers. The tubers were incubated at 26C in the
                     dark for 2-3 weeks prior to sprouting. The eyes were
                     frozen in liquid nitrogen immediately upon removal from
                     tubers."
ORIGIN

Alignment Scores:
Pred. No.:                2.72e-25        Length:          757
Score:                    1065.00         Matches:         200
Percent Similarity:       89.16%          Conservative:    22
Best Local Similarity:    80.32%          Mismatches:      27
Query Match:              30.84%          Indels:          0
DB:                       12              Gaps:            0

US-10-086-464-2 (1-647) x BG596561 (1-757)

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db          1 GCAGTTAAACAGCTTAAGGCTGGAAGTGGACAAGGGGAACGTGAATTTCAGGCGGAAGTT 60

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 GAGATTATTAGCCGAGTACATCACAAGCATCTTGTGTCTCTTGTTGGATACTGCATTACT 120

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||:::||||||||||||||||||||||||||||||   ||||||   ||||||
Db        121 GGGGCTCAGAGACTGCTTGTTTATGAGTTTGTTCCAAACAATACTTTGGAATTTCATTTA 180

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||:::|||||||||   ::::::|||      ||||||||||||||||||||||
Db        181 CACGGAAAGGGAAGGCCTCCTTTGGATTGGCCAATACGGCTAAAGATTGCTCTAGGGTCA 240

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||:::||||||||||||||||||   ||||||||||||||||||||||||
Db        241 GCTAAAGGACTGGCATATCTGCATGAAGACTGCCAACCGAAAATCATTCACCGTGATATC 300

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||:::|||||||||||||||||||   ||||||||||||||||||||||||||||
Db        301 AAGGCAGCTAATATACTTATCGACTTTAATTTTGAGGCTAAGGTTGCTGATTTTGGACTT 360

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||:::   ||||||   ||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAGCTAACTTCTGATGTTAATACTCATGTCTCCACCAGAGTGATGGGAACCTTTGGG 420

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||:::|||||||||||||||:::|||||||||||||||||||||
Db        421 TATTTGGCTCCAGAATATGCTTCCTCTGGAAAGCTTACAGACAAGTCAGACGTATTCTCC 480
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Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||:::|||||||||||||||||||||||||||||||||||||||||||:::
Db        481 TTTGGTGTAATGCTTCTTGAGTTGATAACTGGACGTCGGCCTGTTGACTCTACTCAATCA 540

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              |||::::::|||||||||||||||||||||||||||||||||    ||||||   |||
Db        541 TACATCGAAGATAGTTTGGTGGACTGGGCACGTCCATTACTCACACGAGCTTTAGAAGAT 600

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
                  |||:::   |||   |||   ::::::   |||   |||:::      ||||||
Db        601 GAAAAGTTTGATACCCTTGTTGATCGTCGGCTAGAAAATGATTATAACCATAATGAGATG 660

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||||   ||||||||||||||||||||||:::|||||||||||||
Db        661 GCTCGCATGGTTGCTTGTTGTGCTGCTTGTGTGCGTCATTCAGCAAAGCGTAGACCACGA 720

Qy        541 MetSerGlnIleValArgAlaLeuGlu 549
              |||:::|||::::::||||||||||||
Db        721 ATGACACAGGTTCTCCGAGCCTTGGAA 747

RESULT 8
CB655196
LOCUS       CB655196                731 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  OSJNEc08F21.f OSJNEc Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNEc08F21 5', mRNA sequence.
ACCESSION   CB655196
VERSION     CB655196.1  GI:29658921
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 08  row: F  column: 21
            Seq primer: gta aaa cga cgg cca gtg.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="OSJNEc08F21"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEc"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                     XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
ORIGIN

Alignment Scores:
Pred. No.:              3.05e-25        Length:         731
Score:                  1063.00         Matches:        199
Percent Similarity:     91.36%          Conservative:   23
Best Local Similarity:  81.89%          Mismatches:     21
Query Match:            30.78%          Indels:         0

DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x CB655196 (1-731)

Qy        311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db          1 CAGGGAGAGCGTGAATTCCAGGCGGAGGTTGAGATTATCAGCAGAGTACATCACAAACAT 60

Qy        331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
              ||||||||||||||||||||||||||:::|||    ||||||||||||||||||||||
Db         61 CTCGTCTCCTTGGTTGGTTATTGCATTTCTGGGGGCAAGAGATTGCTTGTCTATGAGTTT 120

Qy        351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              ||||||||||||   ||||||   ||||||||||:::||||||||||||||||||||||
Db        121 GTCCCCAACAACACATTGGAATTCCACTTGCACGGAAAAGGCCGACCAACAATGGAGTGG 180

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
              ||||||||||||||||||||||||:::|||||||||||:::||||||||||||||||||
Db        181 CCCACAAGACTAAAGATTGCTTTGGGAGCTGCAAAGGGTTTAGCTTATCTTCATGAAGAC 240

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::|||||||||||||||||||||||||||||||||||||||:::||||||||
Db        241 TGCCATCCTAAGATCATCCATCGTGATATTAAGGCGTCAAACATTCTTCTTGATTTTAAG 300

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||:::|||||||||||||||||||||||||||||      ||||||   |||||||||
Db        301 TTTGAATCTAAGGTTGCTGATTTTGGACTTGCTAAGTTCACCAGTGATAATAACACTCAT 360

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        361 GTTTCGACAAGAGTAATGGGCACTTTTGGATATCTAGCACCAGAGTACGCATCTTCTGGC 420

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              ||||||||||||||||||||||||||:::|||||||:::||||||||||||||||||||
Db        421 AAGCTCACTGAGAAATCAGATGTCTTCTCCTATGGAGTTATGCTTCTTGAGTTAATAACT 480

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||||||||   :::      |||:::||||||||||||||||||||||||
Db        481 GGTCGTCGGCCAGTTGATACAAGTCAAACATATATGGATGACAGCTTGGTTGACTGGGCA 540

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
              ||||||||||||   :::|||   |||   |||::::::|||   |||   |||   :::
Db        541 AGGCCTTTACTGATGCAAGCACTTGAGAATGGTAACTACGAGGAGTTAGTAGATCCTCGG 600

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
              :::        ::::::      ||||||||||||||:::||||||||||||||||||
Db        601 CTTGGGAAGGATTTCAATCCCAATGAGATGGCGAGAATGATTGCTTGTGCAGCTGCATGC 660

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGly 550
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        661 GTACGCCATTCCGCTCGTCGTCGCCCACGCATGAGCCAGGTTGTCCGGGCTTTGGAAGGT 720

Qy        551 AsnValSer 553
              :::||||||
Db        721 GACGTGTCT 729

RESULT 9
BG441204
LOCUS       BG441204                692 bp    mRNA    linear   EST 15-MAR-2001
DEFINITION  GA__Ea0012C15f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0012C15f, mRNA sequence.
ACCESSION   BG441204
VERSION     BG441204.1  GI:13350856
KEYWORDS    EST.
SOURCE      Gossypium arboreum
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
            Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
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            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Gossypium arboreum"
                     /mol_type="mRNA"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0012C15f"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
                     /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              9.38e-25        Length:         692
Score:                  1047.00         Matches:        198
Percent Similarity:     94.71%          Conservative:   17
Best Local Similarity:  87.22%          Mismatches:     12
Query Match:            30.32%          Indels:         0
DB:                     12              Gaps:           0

US-10-086-464-2 (1-647) x BG441204 (1-692)

Qy        247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
              ||||||||   ||||||||:::   |||||||||||||||||||||||:::||||||
Db         11 CTTCCGCCTGCGTCACCTGGTATTTCCTTAGGTTTCTCGAAAAGCACTTTTAGCTATGAA 70

Qy        267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
              ||||||||||||||||||:::||||||||||||   ||||||||||||||||||||||
Db         71 GAATTAGCGAGAGCAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT 130

Qy        287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        131 GGGTACGTACACAAAGGAGTTCTCCCTAATGGGAAGGAAGTAGCAGTAAAGCAACTCAAG 190

Qy        307 ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgVal 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTGGAAGTGGGCAAGGCGAGAGAGAATTTCAGGCTGAAGTTGAGATCATTAGCCGCGTC 250

Qy        327 HisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeu 346
              ||||||:::|||||||||||||||||||||||||||:::|||      |||:::|||
Db        251 CATCACAAACATCTCGTCTCATTGGTCGGATACTGTATTTCTGGGACAATAAGAATGCTT 310

Qy        347 ValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgPro 366
              ||||||||||||||||||||||   ||||||   ||||||||||:::||||||
Db        311 GTTTATGAGTTTGTTCCAAACAACACCTTGGAGTTTCACTTGCATGGGAAGGGGCGACTG 370

Qy        367 ThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyr 386
              ||||||:::|||   ||||||:::||||||||||||||||||||||||:::|||
Db        371 ACCATGGATTGGCCGACAAGGATGAAAATTGCTTTAGGATCTGCAAAAGGACTGGCATAT 430

Qy        387 LeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 406
              ||||||||||||||:::|||||||||||||||||||||||||:::|||||||||
Db        431 CTTCATGAAGATTGTCATCCTAAGATCATTCACCGTGATATTAAGGCCGCTAATATTCTG 490

Qy        407 IleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAsp 426
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TTGGATTTCAAGTTTGAAGCAAAGGTTGCTGATTTTGGACTAGCGAAAATTGCTTCCGAT 550

Qy        427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyr 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTCAACACGCACGTCTCCACCAGGGTGATGGGTACTTTCGGGTATTTAGCCCCTGAGTAT 610

Qy        447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeu 466
              |||:::|||||||||||||||:::|||||||||||||||||||||||||:::||||||
Db        611 GCTTCAAGTGGAAAGCTCACTGATAAATCAGATGTTTTCTCCTTCGGGGTCATGCTTTTG 670

Qy        467 GluLeuIleThrGlyArgArg 473
              |||||||||||||||   |||
Db        671 GAGTTGATTACCGGTCACAGA 691

RESULT 10
CD839231
LOCUS       CD839231                723 bp    mRNA    linear   EST 10-JUL-2003
DEFINITION  RFO2.114I04F010529 RFO2 Brassica napus cDNA clone RFO2114I04, mRNA
            sequence.
ACCESSION   CD839231
VERSION     CD839231.1  GI:32521171
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .723
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="samourai (restored line)"
                     /db_xref="taxon:3708"
                     /clone="RFO2114I04"
                     /tissue_type="anthers"
                     /clone_lib="RFO2"
ORIGIN

Alignment Scores:
Pred. No.:              3.37e-24        Length:         723
Score:                  1030.00         Matches:        199
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.83%          Indels:         0
DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x CD839231 (1-723)

Qy        449 SerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeu 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTGCTTTTGGAGCTC 61

Qy        469 IleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAsp 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATTACCGGGCGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTTGAC 121

Qy        489 TrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGAGGGTTTAGCTGAT 181

Qy        509 AlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCAAAGATGAATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGTGCTGCG 241
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Qy        529 AlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeu 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATTGTGCGTGCGTTA 301

Qy        549 GluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnVal 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GAAGGAAATGTATCACTGTCAGATCTTAACGAAGGGATGAGACCAGGTCAAAGCAATGTA 361

Qy        569 TyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLys 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAG 421

Qy        589 LysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsn 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAGTTTAGGAAAATGGCTCTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAAT 481

Qy        609 ProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CCGACCAGCGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 541

Qy        629 GluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCTT 598

RESULT 11
AY108241
LOCUS       AY108241                1053 bp    mRNA    linear   HTC 16-OCT-2002
DEFINITION  Zea mays PCO134818 mRNA sequence.
ACCESSION   AY108241
VERSION     AY108241.1  GI:21211319
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1053)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1053)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1053
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:637889"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

Alignment Scores:
Pred. No.:          5.61e-24      Length:       1053
Score:              1027.50       Matches:      203
Percent Similarity:     79.93%          Conservative:  28
Best Local Similarity:  70.24%          Mismatches:    46
Query Match:            29.76%          Indels:        12
DB:                     11              Gaps:          4

US-10-086-464-2 (1-647) x AY108241 (1-1053)

Qy        365 ArgProThrMetGluTrpSerThrArgLeuLysIle-AlaLeuGlySerAlaLysGlyLe 384
              ||||||      ||||||      ||||||||||||    ||||||:::||||||||||||
Db          6 CGTCCG------GAGTGGCCTGCTAGATTAAAGATCATGTTTGGGTGCTGCCAAGGGTTT 59

Qy        384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404
              |:::||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         60 AGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCATCTAA 119

Qy        404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424
              |||||||:::||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        120 CATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGATTTTGGACTTGCAAAGTTCAC 179

Qy        424 aSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaPr 444
              :::|||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTGGCACC 239

Qy        444 oGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVa 464
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||::
Db        240 TGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGAGTCAT 299

Qy        464 lLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAs 484
              :||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db        300 GCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATGGATGA 359

Qy        484 pSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGl 504
              ||||||||||||||||||||||||||||||    ||||||   |||   |||::::::::
Db        360 CAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAATATGA 419

Qy        504 uGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVa 524
              :   |||   |||   ::::::         ::::::       ||||||||||||||::
Db        420 TGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGAATGAT 479

Qy        524 lAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db        480 AGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGTCAGGT 539

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564
              :|||||||||||||||||||||||||||||    ||||||||||||||:::|||||||||
Db        540 CGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGGCCTGG 599

Qy        564 yGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAs 584
              |   |||      :::   ||||||      |||:::|||||||||||   ||||||||
Db        600 CCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAGTACAA 656

Qy        584 nGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGl 604
              ||||||||||||||||||:::|||||||||                         :::
Db        657 CGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACCAGCAG 710

Qy        604 yGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGl 624
              :::||||||   |||||||||:::||||||      ||||||   ||||||||||||||||
Db        711 CCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGCGAGGG 770

Qy        624 yGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly-------------- 639
              |      |||:::||||||||||   |||   :::|||:::   |||
Db        771 CCACCAGACGCAAGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGTGGCTA 830

Qy        640 ----GlnGlyTyrSerGlyProSer 646
                  ||||||||||||   |||
Db        831 CAGCTCAGGATACAGCGGAGCCTCG 855

RESULT 12
AY108243
LOCUS       AY108243                1016 bp    mRNA    linear   HTC 16-OCT-2002
DEFINITION  Zea mays PCO134814 mRNA sequence.
ACCESSION   AY108243
VERSION     AY108243.1  GI:21211321
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KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1016)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1016)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1016
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:637888"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

Alignment Scores:
Pred. No.:              6.53e-24        Length:         1016
Score:                  1025.00         Matches:        200
Percent Similarity:     82.14%          Conservative:   30
Best Local Similarity:  71.43%          Mismatches:     42
Query Match:            29.68%          Indels:         8
DB:                     11              Gaps:           4

US-10-086-464-2 (1-647) x AY108243 (1-1016)

Qy        373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
              ||||||||||||||||||||:::|||||||||||:::||||||||||||||||||||:::
Db          3 AGATTAAAGATCGCTCTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCAT 62

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db         63 CCAAAGATCATCCACCGCGACATTAAGGCATCTAACATTCTTCTTGACTTCAAATTTGAA 122

Qy        413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
              |||   ||||||||||||||||||||||      :::|||   ||||||||||||||||
Db        123 GCTATGGTTGCTGACTTTGGACTTGCAAAGTTCACTACTGATAACAACACCCATGTGTCA 182

Qy        433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACAAGAGTAATGGGCACCTTTGGGTATTTGGCACCCGAGTATGCAGCATCTGGCAAGCTC 242

Qy        453 ThrGluLysSerAspValPheSerPheGlyValValLeuGluLeuIleThrGlyArg 472
              |||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        243 ACAGAAAAATCCGATGTATTTTCTTTCGGAGTCATGCTTCTTGAGCTTATTACTGGGCGG 302

Qy        473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
              ||||||:::|||           |||:::||||||||||||||||||||||||||||||
Db        303 CGACCAATTGACACAACCCAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCA 362

Qy        493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
              ||||||   ||||||   |||   |||:::::::::   |||   |||   ::::::
Db        363 TTACTGATGAGAGCGCTCGAGGATGGTGAATATGATGCTTTGGTGGATCCTCGGCTCGGA 422

Qy        513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
                  ::::::      ||||||||||||||||:::||||||||||||||||||||||||
Db        423 AAGGACTTCAATCCTAACGAGATGGCAAGAATGATAGCCTGTGCGGCTGCGTGCGTACGC 482

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552
              ||||||||||||||||||||||||||||||:::||||||||||||||||||:::|||
Db        483 CATTCCGCACGTCGTCGGCCACGAATGAGTCAGGTCGTTCGGGCTCTGGAAGGCGACGTG 542

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572
              ||||||   ||||||||||||||:::|||||||||   |||      :::   ||||||
Db        543 TCTTTGGAGGACCTTAATGAAGGTGTTCGACCTGGCCATAGCCGCTTCTTTGGGTCATAT 602

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592
                  |||:::|||||||||||   ||||||||||||||||||:::||||||||||||
Db        603 ---AGCAGCTCTGATTACGATTCCGGGCAGTACAACGAGGACATGCAGAAGTTCAGGAAG 659

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612
                  |||                  |||   ::::::   :::||||||   |||||||||:::
Db        660 ACGGCGTTCAATAACAACACCTACACCAGCAGC---CAATACAGCGCGCCAACCAGTGAA 716

Qy        613 TyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMet---Glu 631
              ||||||   ||||||||||||||||||||||:::   |||:::||||||   |||
Db        717 TACGGCCAGGTGCCGTCTGGATCAAGCAGCGAGGGCCGCCAGACGCAGGAGATGGAGGAG 776

Qy        632 MetGlyLysIleLysArgThrGly----------------GlnGlyTyrSerGlyProSer 646
                  |||   :::|||:::   |||                   ||||||||||||   |||
Db        777 TCGGGTGCAGTGAAGAAAGGTGGCTACAGCGGCTACAGCTCCGGATACAGCGGAGCCTCG 836

RESULT 13
BM358715
LOCUS       BM358715                 666 bp    mRNA    linear   EST 09-JAN-2002
DEFINITION  GA__Ea0012D16r Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0012D16r, mRNA sequence.
ACCESSION   BM358715
VERSION     BM358715.1  GI:18099461
KEYWORDS    EST.
SOURCE      Gossypium arboreum
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
            Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total High Quality bases = 646
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 666.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Gossypium arboreum"
                     /mol_type="mRNA"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0012D16r"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:

Pred. No.:	7.55e-24	Length:	666
Score:	1018.00	Matches:	191
Percent Similarity:	95.41%	Conservative:	17
Best Local Similarity:	87.61%	Mismatches:	10
Query Match:	29.48%	Indels:	0
DB:	12	Gaps:	0

US-10-086-464-2 (1-647) x BM358715 (1-666)

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Qy       247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
Db        11 CTTCCGCCTCCGTCACCTGGTATTTCCTTAGGTTTCTCGAAAAGCACTTTTAGCTATGAA 70

Qy       267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
Db        71 GAATTAGCGAGAGCAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT 130

Qy       287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
Db       131 GGGTACGTACACAAAGGAGTTCTCCCTAATGGGAAGGAAGTAGCAGTAAAGCAACTCAAG 190

Qy       307 ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgVal 326
Db       191 GCTGGAAGTGGGCAAGGCGAGAGAGAATTTCAGGCTGAAGTTGAGATCATTAGCCGCGTC 250

Qy       327 HisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeu 346
Db       251 CATCACAAACATCTCGTCTCATTGGTCGGATACTGTATTTCTGGGACAATAAGAATGCTT 310

Qy       347 ValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgPro 366
Db       311 GTTTATGAGTTTGTTCCAAACAACACCTTGGAGTTTCACTTGCATGGGAAGGGGCGACTG 370

Qy       367 ThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyr 386
Db       371 ACCATGGATTGGCCGACAAGGATGAAAATTGCTTTAGGATCTGCAAAAGGACTGGCATAT 430

Qy       387 LeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 406
Db       431 CTTCATGAAGATTGTCATCCTAAGATCATTCACCGTGATATTAAGGCCGCTAATATTCTG 490

Qy       407 IleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAsp 426
Db       491 TTGGATTTCAAGTTTGAAGCAAAGGTTGCTGATTTTGGACTAGCGAAAATTGCTTCCGAT 550

Qy       427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyr 446
Db       551 GTCAACACGCACGTCTCCACCAGGGTGATGGGTACTTTCGGGTATTTAGCCCCTGAGTAT 610

Qy       447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVal 464
Db       611 GCTTCAAGTGGAAAGCTCACTGATAAATCAGATGTTTTCTCCTTCGGGGTCATG 664
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RESULT 14
CA072174
LOCUS CA072174 695 bp mRNA linear EST 23-SEP-2003
DEFINITION SCCCAM1004A11.g AM1 Saccharum officinarum cDNA clone SCCCAM1004A11 5', mRNA sequence.
ACCESSION CA072174
VERSION CA072174.1 GI:34924325
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 695)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 004 row: A column: 11
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .695
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCCAM1004A11"
/lab_host="DH10B"
/clone_lib="AM1"
/note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Alignment Scores:

Pred. No.:	1.13e-23	Length:	695
Score:	1013.00	Matches:	195
Percent Similarity:	91.85%	Conservative:	19
Best Local Similarity:	83.69%	Mismatches:	16
Query Match:	29.34%	Indels:	3
DB:	13	Gaps:	1

US-10-086-464-2 (1-647) x CA072174 (1-695)

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Qy       271 AlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHis 290
Db         4 GCAACCAATGGGTTTTCTGACGCTAATCTGCTGGGGCAAGGCGGTTTTGGGTTTGTTCAC 63

Qy       291 LysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGly 310
Db        64 AAAGGAGTGCTACCAAATGGCACAGAGGTTGCTGTTAAGCAGTTAAGAGATGGAAGTGGC 123

Qy       311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
Db       124 CAGGGAGAACGCGAGTTTCAGGCAGAGGTTGAGATTATCAGCAGAGTACATCACAAGCAT 183

Qy       331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
Db       184 CTTGTATCCTTGGTCGGCTATTGCATTTCTGGAGCCAACAGGTTGCTCGTCTACGAGTTT 243

Qy       351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
Db       244 GTTCCAAACAATACATTGGAATTCCACTTACATGGAAAAGGCAGACCAACCTTGGATTGG 303

Qy       371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
Db       304 CCGACAAGACTAAAAATTGCTCTGGGTTCTGCGAAGGGATTGGCATATCTTCATGAAGAT 363

Qy       391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
Db       364 TGCCATCCTAAGATCATTCATCGTGACATAAAGGCCTCAAATATTCTTCTTGATCTAAGA 423
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Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db        424 TTTGAAGCTAAGGTGGCAGATTTTGGACTTGCAAAATTCACTTCTGATACAAACACCCAT 483

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTTTCAACCAGAGTAATGGGCACATTTGGGTACCTAGCACCTGAGTATGCTGCTTCTGGC 543

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db        544 AAGCTCACTGAGAAATCAGATGTCTTCTCTTTTGGAGTAATGCTTCTTGAGCTAATAACT 603

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||        |||:::        ||||||:::|||   |||||||||
Db        604 GGGCGGCGTCCT------GGTAATTCAAGACAGGCAGATGACAACTTGGGTGACTGGGCA 657

Qy        491 Arg-ProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
              ||| ||||||:::|||:::|||   |||   |||:::
Db        658 AGGGCCTTTGATGAATAAAGCATTTGAGGATGGTAAT 694

RESULT 15
BU099573
LOCUS       BU099573                715 bp    mRNA    linear   EST 29-AUG-2002
DEFINITION  WHE3309_A09_A17ZS Chinese Spring wheat drought stressed root cDNA
            library Triticum aestivum cDNA clone WHE3309_A09_A17, mRNA
            sequence.
ACCESSION   BU099573
VERSION     BU099573.1  GI:22547372
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 715)
  AUTHORS   Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D.,
            Lazo,G.R., Nguyen H.T., Pham,J., Rausch,C.J., Turuspekov,Y.,
            Wilson,C., Woo,J. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Chinese Spring drought stressed root cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequences have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: SK primer.
FEATURES             Location/Qualifiers
     source          1. .715
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE3309_A09_A17"
                     /tissue_type="root"
                     /dev_stage="Full tillering stage"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Chinese Spring wheat drought stressed root
                     cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown under
                     normal conditions, then drought stressed to 80%, 70% and
                     60% RWC at Texas Tech University (D. Zhang in HT Nguyen
                     lab). Total RNA was prepared separately for roots
                     collected at the three different drought conditions. Equal
                     amounts of total RNA were pooled from all three samples,
                     poly(A) RNA were purified, one cDNA library was made, and
                     the cDNA clones were in vivo excised to give pBluescript
                     SK(-) phagemids in the TJ Close lab at the University of
                     California, Riverside (Fenton, Turuspekov). Plasmid DNA
                     preparations and DNA sequencing were performed in the OD
                     Anderson lab (all other authors)."
ORIGIN

Alignment Scores:
Pred. No.:              1.04e-22        Length:         715
Score:                  983.00          Matches:        184
Percent Similarity:     89.70%          Conservative:   25
Best Local Similarity:  78.97%          Mismatches:     24
Query Match:            28.47%          Indels:         0
DB:                     13              Gaps:           0

US-10-086-464-2 (1-647) x BU099573 (1-715)

Qy        276 SerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPro 295
              |||:::|||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db         11 TCCGATGCTAATCTTCTCGGGCAAGGTGGCTTTGGATTTGTTCACAAAGGAGTGCTGCCA 70

Qy        296 SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGlu 315
              |||   ||||||||||||||||||||||:::   ||||||||||||||||||||||||||
Db         71 GATGGCACAGAAGTTGCTGTGAAGCAATTAAGAGATGGAAGTGGGCAGGGAGAGCGTGAG 130

Qy        316 PheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVal 335
              ||||||||||||||||||||||||||||||||||||:::|||||||||:::||||||
Db        131 TTCCAGGCAGAGGTTGAGATTATCAGCCGAGTACATCATAAACATCTCGTGACATTGGTT 190

Qy        336 GlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsn 355
              ||||||||||:::       ||||||||||||||||||||||||||||||||||||
Db        191 GGTTATTGCATTTCTGAAGACAAGAGGTTGCTTGTCTATGAGTTTGTTCCCAATAACACG 250

Qy        356 LeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLys 375
              ||||||   |||:::||||||          |||||||||:::|||   :::||||||:::
Db        251 TTAGAATTCCATATACATGGAAGGCGTGGACCAACTATGGACTGGCCTTCAAGACTACGT 310

Qy        376 IleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIle 395
              ||||||||||||||||||||||||||:::|||||||||||||||||:::||||||||||
Db        311 ATTGCTTTGGGTTCTGCGAAGGGATTGGCGTATCTTCACGAAGACTGCCATCCAAAGATC 370

Qy        396 IleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysVal 415
              ||||||||||||||||||||||||||||||:::|||::::::   ||||||||||||
Db        371 ATTCATCGTGACATAAAGGCATCAAATATTCTTCTGGATTACAGATGTGAAGCTAAGGTG 430

Qy        416 AlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVal 435
              ||||||||||||||||||||:::   ||||||   ||||||||||||||||||||||||
Db        431 GCAGATTTTGGACTTGCAAAGTTAACCTCTGATAATAACACTCATGTTTCCACCAGAGTA 490

Qy        436 MetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLys 455
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        491 ATGGGCACATTTGGGTACCTTGCACCAGAGTATGCTTCTTCTGGCAAGCTAACTGAGAAA 550

Qy        456 SerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVal 475
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db        551 TCAGATGTCTTTTCTTTTGGAGTAATGCTTCTCGAGTTAATAACTGGGCGCCGTCCTGTA 610

Qy        476 AspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsn 495
              :::         ::::::||||||||||||||||||||||||||||||||||:::
Db        611 AGTTCAAAACAAGCGCATATGGATGACAGCTTGGTTGACTGGGCAAGGCCTTTGATGACA 670

Qy        496 ArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
              :::|||   |||   |||:::   :::   |||   |||
Db        671 CAAGCACTCGAGGATGGTAATCACGATGCTTTAGTGGAT 709


Search completed: April 25, 2004, 00:59:49
Job time : 3628 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 24, 2004, 20:30:41 ; Search time 133 Seconds
(without alignments)
2699.648 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	756	21.9	3239	4	US-09-228-986-9	Sequence 9, Appli
2	744.5	21.6	1593	4	US-09-602-472A-1	Sequence 1, Appli
3	740	21.4	2868	4	US-09-228-986-4	Sequence 4, Appli
4	712	20.6	1488	4	US-09-579-182-4	Sequence 4, Appli
5	703.5	20.4	2513	4	US-09-228-986-13	Sequence 13, Appl
6	678	19.6	2432	4	US-09-228-986-7	Sequence 7, Appli
7	667.5	19.3	1559	4	US-09-602-472A-3	Sequence 3, Appli
8	604.5	17.5	4104	3	US-08-881-706-1	Sequence 1, Appli
9	602	17.4	1224	4	US-09-579-182-3	Sequence 3, Appli
10	600.5	17.4	3097	4	US-09-228-986-11	Sequence 11, Appl
11	581.5	16.8	3590	1	US-08-587-889-1	Sequence 1, Appli
12	581.5	16.8	3590	4	US-09-016-434-1093	Sequence 1093, Ap
13	581.5	16.8	3590	5	PCT-US96-09193-1	Sequence 1, Appli
14	578	16.7	2114	4	US-09-602-472A-5	Sequence 5, Appli
15	575	16.7	2749	1	US-08-265-628-1	Sequence 1, Appli
16	572	16.6	2571	1	US-07-717-331F-9	Sequence 9, Appli
17	572	16.6	2833	1	US-07-717-331F-1	Sequence 1, Appli
18	567	16.4	1554	2	US-08-587-680A-24	Sequence 24, Appl
19	566.5	16.4	2389	4	US-09-228-986-1	Sequence 1, Appli
20	562	16.3	2336	4	US-09-228-986-10	Sequence 10, Appl
21	559.5	16.2	2638	4	US-09-228-986-8	Sequence 8, Appli
22	546	15.8	2749	1	US-07-717-331F-4	Sequence 4, Appli
23	545	15.8	966	1	US-08-447-185-2	Sequence 2, Appli
24	545	15.8	2443	1	US-08-447-185-3	Sequence 3, Appli
25	543	15.7	2686	4	US-09-228-986-3	Sequence 3, Appli
26	531.5	15.4	5733	2	US-08-473-553A-1	Sequence 1, Appli
27	486	14.1	2943	4	US-09-503-922-2	Sequence 2, Appli
28	460.5	13.3	2649	4	US-09-228-986-12	Sequence 12, Appl
29	430	12.5	2568	4	US-09-228-986-2	Sequence 2, Appli
c 30	401	11.6	1926	4	US-09-249-585A-2	Sequence 2, Appli
c 31	401	11.6	1926	4	US-09-410-399-3	Sequence 3, Appli
c 32	401	11.6	2580	3	US-09-050-863-2	Sequence 2, Appli
c 33	401	11.6	2580	4	US-09-359-081-2	Sequence 2, Appli
34	401	11.6	5452	2	US-09-130-114-1	Sequence 1, Appli
35	401	11.6	8705	4	US-09-647-344A-14	Sequence 14, Appl
c 36	401	11.6	9600	3	US-08-910-647-1	Sequence 1, Appli
c 37	401	11.6	9600	4	US-09-620-925-1	Sequence 1, Appli
c 38	401	11.6	10596	1	US-07-884-811-15	Sequence 15, Appl
c 39	401	11.6	10596	1	US-07-885-971-15	Sequence 15, Appl
c 40	401	11.6	10596	1	US-08-087-783A-15	Sequence 15, Appl
c 41	401	11.6	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 42	401	11.6	10596	2	US-08-194-087-15	Sequence 15, Appl
c 43	401	11.6	10596	5	PCT-US93-04648-15	Sequence 15, Appl
44	401	11.6	16080	4	US-09-724-566A-48	Sequence 48, Appl
45	395.5	11.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Alignment Scores:
Pred. No.: 1.88e-23 Length: 3239
Score: 756.00 Matches: 190
Percent Similarity: 51.93% Conservative: 92
Best Local Similarity: 34.99% Mismatches: 132
Query Match: 21.89% Indels: 130
DB: 4 Gaps: 17

US-10-086-464-2 (1-647) x US-09-228-986-9 (1-3239)

```
Qy          89 ProProAlaProVal-ThrProProThrArgAsnProProProSerValProGlyProPr 108
               ||||||   |||       |||   |||   :::|||||||||   :::        ||
Db        1759 CCTCCCAAACCATTCGGCCCCTATTACTTCATCGCCTCCCCCTATGCTTTT-------CC 1811

Qy         108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                |   |||            ||||||:::
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```
Db       1812 AGACAAT------------GGAGGAACC------------------------------ 1827

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148

Db       1828 -------------GCCATAAGCAAAGGTGTGATAGTTGGGATCGCTATTGGCGGCACGGT 1874

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db       1875 TCTGGTTCTTGGCCTTGTTGTATTAGGGTTATATGCTATTCGACAAAAGAAACGGGCGGA 1934

Qy        168 uGluAspAlaTyrTyrValProProPro------------ProProProGlyProLysAl 184

Db       1935 GAAA---GCTCTCGAGTTGAGCAGACCCTTCGCATCCTGGGCACCCAGTGGGAAAGATAG 1991

Qy        184 aGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSe 204

Db       1992 CGGAGGAGCGCCACAACTGAAAGGAGCACGATGG------------------------- 2025

Qy        204 rAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGlnPr 224

Db       2025 ------------------------------------------------------------ 2025

Qy        224 oProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAspAr 244

Db       2025 ------------------------------------------------------------ 2025

Qy        244 gProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheTh 264

Db       2026 ------------------------------------------------------TTCTC 2030

Qy        264 rTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGl 284

Db       2031 CTATGATGAACTTAAGAGGTGCACCAATAATTTCTCCGATAGCAATGAATTAGGCTTCGG 2090

Qy        284 yGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGl 304

Db       2091 AGGATACGGAAAGGTGTACAGGGGAGTTCTTCCTGATGGTCATATATTAGCAATCAAAAG 2150

Qy        304 nLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSe 324

Db       2151 AGCTCAGCAGGGGTCGATGCAGGGTGCAACCGAGTTCAAGACAGAAATCGAGCTGCTTTC 2210

Qy        324 rArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysAr 344

Db       2211 GCGGGTTCATCACAAGAATCTTGTTGGCCTCATAGGATTCTGTTTCGAGCAAGGAGAGCA 2270

Qy        344 gLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGl 364

Db       2271 GATGTTGGTCTATGAATATATGCCTAACGGGACGCTCAGGGATAGCTTGACAGGAAAATC 2330

Qy        364 yArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLe 384

Db       2331 AGGCATTTATCTTGATTGGAAGAGGAGGCTTCGTATAGCTCTAGGTTCGGCTAGAGGACT 2390

Qy        384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404

Db       2391 AGCTTATCTGCACGAACTCGCGAATCCTCCAATTATCCACAGAGATGTCAAGTCCACCAA 2450

Qy        404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424

Db       2451 TATCTTGTTGGACGAACATCTGACGGCCAAAGTCGCGGATTTCGGTTTGTCCAAACTGGT 2510

Qy        424 aSerAspThrAsnThr---HisValSerThrArgValMetGlyThrPheGlyTyrLeuAl 443

Db       2511 ATCGGACAGCGGGAAGGGGCACGTTTCGACGCAAGTGAAAGGCACGCTGGGCTATTTGGA 2570

Qy        443 aProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVa 463

Db       2571 TCCCGAATACTACATGAGTCAACAGCTGACAGAAAAGAGCGATGTGTACAGCTTCGGGGT 2630

Qy        463 lValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAs 483

Db       2631 GGTCATGCTTGAGCTCATCACTGCAAAGCAACCGATTGAGAAGGGCAAGTATGTCGTCCG 2690

Qy        483 pAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPh 503

Db       2691 CGAG--------------ATTCGCACCGCCATGGACAAGAACGACCAG------GACTA 2729

Qy        503 eGluGly---------LeuAlaAspAlaLysMetAsnAsn---GlyTyrAspArgGluGl 519

Db       2730 CTACGGCGTGAGGGAAATGATGGACCCGTCCATGAGGAGCATGGGCTAC---CTCGTCGG 2786

Qy        519 uMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPr 539

Db       2787 GTTCAGCAGGTTCTTGGATTTGGCGATGCGATGTGTCGAGGAGTCGGCTGCGGACCGCCC 2846

Qy        539 oArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGl 559

Db       2847 CACAATGAGCGAGGTGGTGAAGGCGATCGAGACCATGTTGCAG------------AACGA 2894

Qy        559 uGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAs 579

Db       2895 TGGGATACACACCAACTCGACGTCCGCATCGTCGTCG---------GCGACGGACTTTGG 2945

Qy        579 pSerSerGln-----------------TyrAsnGluAspMetLysLysPheArgLysMe 593

Db       2946 GTCGACGAAGGGCGCTCCTCGGCATCCGTACAACGATGCCTTACCCAAG----------- 2994

Qy        593 tAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTy 613

Db       2995 -------AAGGAAGTTAGCTATAGCGATTCCTTTGATTATAGT---------GGTGGATA 3038

Qy        613 rGlyLeu 615

Db       3039 TGGACTA 3045
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RESULT 2
US-09-602-472A-1
; Sequence 1, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
US-09-602-472A-1

Alignment Scores:

Pred. No.:	2.9e-23	Length:	1593
Score:	744.50	Matches:	172
Percent Similarity:	57.07%	Conservative:	66
Best Local Similarity:	41.25%	Mismatches:	116
Query Match:	21.56%	Indels:	63
DB:	4	Gaps:	9

US-10-086-464-2 (1-647) x US-09-602-472A-1 (1-1593)

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Qy        235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeu 254

Db        181 TCGTCGGGTTCGAAAGACGGGTCGCAGGGTCAGATT------------------------ 216

Qy        255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274

Db        217 ------------GCTGCTCATACATTCACTTTCCGGGAGCTTGCAGCTGCAACAAACAAT 264
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Qy        275 PheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294
Db        265 TTTAGCCCTGATTGTTTGCTAGGAGAAGGAGGGTTTGGCCATGTGTATAGAGGACGGCTT 324

Qy        295 Pro---SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGlu 313
Db        325 CCGGGCAGCGGTCAGATTGTAGCTGTCAAACAATTGGATAGGAACGGGCTGCAGGGTAAC 384

Qy        314 ArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSer 333
Db        385 CGTGAATTTCTCGTAGAAGTTCTTATGCTCAGCCTTTTACATCATCCCAATTTGGTGAAT 444

Qy        334 LeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsn 353
Db        445 TTAATCGGATACTGTGCTGATGGTGACCAAAGACTTCTTGTTTATGAATTCATGCCATTG 504

Qy        354 AsnAsnLeuGluLeuHisLeuHisGly------GluGlyArgProThrMetGluTrpSer 371
Db        505 GGATCGTTAGAAGATCATCTTCATGATCTCCCACCAGAAAAAGAAGCGTTAGATTGGAAC 564

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391
Db        565 ACAAGAATGAAGATAGCGGCTGGTGCAGCTCGAGGTTTGGAATTTCTTCACGATAAGGCT 624

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411
Db        625 AATCCTCCTGTTATTTACAGGGATTTCAAATCATCAAACATTTTGCTCGGTGAGGGATTT 684

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAla---SerAspThrAsnThrHis 430
Db        685 CAACCAAAGCTTTCTGATTTCGGGCTAGCGAAGTTGGGCCCGACGGGAGATAAGTCTCAT 744

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
Db        745 GTATCCACACGGGTCATGGGAACGTATGGTTACTGTGCTCCTGAGTATGCGATGACCGGT 804

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
Db        805 CAACTCACTGTTAAGTCTGATGTGTATAGCTTTGGGGTGGTTTTCTTAGAGCTTATTACA 864

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
Db        865 GGCCGAAAAGCCATTGACAGCAGTGCACCGCAAGGACAGCAGAATCTCGTCACTTGGGCA 924

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
Db        925 CGACCCTTATTCAAC---------GACAGAAGGAAATTTGCAACATTGGCAGACCCCAGG 975

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
Db        976 CTTGAAGGACATTATCCCATGAGGGGTCTGTACCAGGCTCTAGCGGTTGCATCGATGTGC 1035

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeu------ 548
Db       1036 ATCCAAGAACAGGCTGCGGCTCGACCGCTTATAGGAGACGTGGTCACTGCCTTATCTTAT 1095

Qy        548 ------------------------------------------------------------ 548
Db       1096 CTTGCGAACCACACCTATGATCCCAATGCGGCCTCTGGTCAAAGCAACCGGTACAACAAC 1155

Qy        549 ---GluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
Db       1156 GGTGAGAGAACCAGTAGAATTTCAAAGAATGAAGAAGGTGGTGGGTCGGGTCGTAGCAGG 1215

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln-------------- 582
Db       1216 ---TGGGGGGATCTAGAAGGTTCCGACAAAGGAGATTCGCCTCGAGAAACTCAAACTCCA 1272

Qy        583 ------TyrAsnGluAspMet---------------------------------------- 587
Db       1273 AGGATGCTGAATCGAGATCTTGATCGAGAACGGGCTGTTGCTGAGGCTAAAATGTGGGTA 1332

Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGly 604
Db       1333 GAAAAAAGACGACAAAGTGCACAAGGCAGCTTTGATGGGAATGCTAACGGT 1383

RESULT 3
US-09-228-986-4
; Sequence 4, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 2868
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-09-228-986-4

Alignment Scores:
Pred. No.:              7.71e-23        Length:         2868
Score:                  740.00          Matches:        182
Percent Similarity:     50.91%          Conservative:   69
Best Local Similarity:  36.92%          Mismatches:     133
Query Match:            21.43%          Indels:         109
DB:                     4               Gaps:           13

US-10-086-464-2 (1-647) x US-09-228-986-4 (1-2868)

Qy         90 ProAlaProValThrProProThrArgAsnProProProSerValProGlyProPro--- 108
Db        858 CCATGTCCGGGATCTCCTCCTTTTTCTCCTCCTCCTCCGTTTGTACCACCCCCGCCAGTA 917

Qy        109 ------SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerPro 126
Db        918 GCTGGAAGCAATGGAGCAAGGGTGCAGAGCTCTTCC---------------------- 953

Qy        127 ProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGly 146
Db        954 -----------------------AGCACAGGAGCCATTGCTGGGGGAGTAGCTGCAGGT 989

Qy        147 ValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg 166
Db        990 GCTGCCCTCTTATTT---------------------------------------------- 1004

Qy        167 AspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGly 186
Db       1005 ------------------------------------GCAGCTCCTGCAATTGGGTTC 1025

Qy        187 ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHis 206
Db       1026 GCCTGG-----------------TGGCGTCGCAGAAAG---------CCACAGGAGCAC 1058

Qy        207 ValValThrSerLeuProProProProLysAlaProSerProProArgGlnProProPro 226
Db       1058 ------------------------------------------------------------ 1058

Qy        227 ProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProVal 246
Db       1059 ----------------------------------------TTCTTTGATGTACCTGCT 1076

Qy        247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
Db       1077 ------GAGGAGGATCCAGAAGTTCACTTAGGCCAACTTAAG---AGGTTCTCATTACGG 1127

Qy        267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
Db       1128 GAATTACAGGTTGCAACTGATGGTTTTAGCAATAGAAACATTCTTGGCAGAGGTGGTTTT 1187
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Qy        287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
Db       1188 GGAAAGGTGTACAAAGGGCGCCTTGCAGATGGTTCCTTGGTGGCTGTAAAACGTCTGAAG 1247

Qy        307 ---ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArg 325
Db       1248 GAAGAGCGTACACCGGGTGGAGAGTTGCAGTTTCAAACAGAAGTGGAGATGATAAGCATG 1307

Qy        326 ValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeu 345
Db       1308 GCAGTACATAGGAACCTCCTTCGACTACGTGGATTCTGCATGACACCCACTGAACGGCTG 1367

Qy        346 LeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLeuHisGlyGlu 363
Db       1368 CTTGTTTATCCCTACATGGCCAATGGAAGTGTTGCTTCATGCCTACGAGAGAGGGCACAA 1427

Qy        364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db       1428 AATGACCCACCCTTAGATTGGCCAACTCGCAAGCGCATAGCATTGGGTTCTGCAAGAGGT 1487

Qy        384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
Db       1488 CTCTCCTACTTGCATGATCATTGTGATCCTAAGATTATTCACCGGGATGTCAAGGCTGCT 1547

Qy        404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423
Db       1548 AACATCTTACTGGATGAAGAATATGAGGCAGTGGTGGGGGATTTTGGCTTGGCAAAACTT 1607

Qy        424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443
Db       1608 ATGGATTATAAGGACACACATGTTACGACGGCTGTTCGTGGAACCATTGGCCACATAGCA 1667

Qy        444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463
Db       1668 CCTGAGTACCTTTCTACTGGAAAGTCTTCGGAAAAGACAGACGTATTTGGATATGGAATC 1727

Qy        464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAsp 483
Db       1728 ATGTTGCTGGAACTTATTACGGGACAACGGGCATTTGACCTTGCACGTTTAGCAAATGAT 1787

Qy        484 AspSer------LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501
Db       1788 GATGATGTCATGTTGCTTGACTGGGTTAAAGGCCTACTA------------AAAGAGAGA 1835

Qy        502 AspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAla 521
Db       1836 AGGCTTGATATGCTAGTTGATCCTGATCTTAAGAACAATTATGTTGAAGCAGAGGTGGAA 1895

Qy        522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMet 541
Db       1896 CAACTTATTCAAGTTGCATTACTTTGTACACAAGGGTCACCAATGGATAGACCAAAGATG 1955

Qy        542 SerGlnIleValArgAlaLeuGluGlyAsn-ValSerLeuSerAspLeuAsnGluGlyMe 561
Db       1956 TCTGAAGTGGTAAGGATGTTGGAAGGGGATGGCTTAGCTGAGAGATGGGAGGAATGGCAA 2015

Qy        561 tArgProGlyGlnSerAsnValTyrSerSerTyrGly 573
Db       2016 AAGG-----------------TGGAAGTCGTACGGA 2034

RESULT 4
US-09-579-182-4
; Sequence 4, Application US/09579182
; Patent No. 6500628
; GENERAL INFORMATION:
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
;  TITLE OF INVENTION:  PHOSPHATASE HOMOLOGUES AND USES THEREFOR
;  FILE REFERENCE:  MNI-161
;  CURRENT APPLICATION NUMBER: US/09/579,182
;  CURRENT FILING DATE:  2000-05-25
;  NUMBER OF SEQ ID NOS:  7
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;  LENGTH: 1488
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-579-182-4

Alignment Scores:
Pred. No.:                6.04e-22        Length:          1488
Score:                    712.00          Matches:         178
Percent Similarity:       53.07%          Conservative:    73
Best Local Similarity:    37.63%          Mismatches:      160
Query Match:              20.62%          Indels:          62
DB:                       4               Gaps:            14

US-10-086-464-2 (1-647) x US-09-579-182-4 (1-1488)

Qy        205 AspHisValValThrSerLeuProPro--------------ProProLysAlaProSer 219
Db         22 GAACACACGATAAATCCCTTCGCTCCGCTATATTTCCTAAATCCCGATAAATCAAAGTCT 81

Qy        220 ProProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySer 239
Db         82 ------CGACGAGGTCCT---------------------------------------- 93

Qy        240 AspTyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSer 259
Db         94 ------GAACAGAAGAAGGAGCTAACTGCTCCAAAAGAAGGGCCTACTGCGCATATTGCT 147

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
Db        148 GCACAAACCTTTACTTTCCGAGAGTTAGCTGCCGCCACTAAAAACTTTCGACCGGAATGT 207

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu---ProSerGlyLys 298
Db        208 CTTCTTGGAGAAGGAGGTTTCGGACGTGTTTACAAAGGTCGTCTAGAGACCACAGGACAG 267

Qy        299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318
Db        268 ATAGTAGCTGTTAAACAGCTTGATCGAAACGGTCTACAAGGAAACAGAGAGTTTCTTGTA 327

Qy        319 GluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338
Db        328 GAGGTTCTTATGCTGAGCCTTCTGCATCATCCCAATCTTGTGAATTTGATTGGTTATTGT 387

Qy        339 IleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeu 358
Db        388 GCTGATGGGGACCAGCGTCTTCTTGTGTATGAGTATATGCCACTAGGATCATTGGAGGAT 447

Qy        359 HisLeuHisGly------GluGlyArgProThrMetGluTrpSerThrArgLeuLysIle 376
Db        448 CATCTACACGATCTTCCACCTGATAAAGAGCCTCTAGACTGGAGTACTAGAATGACAATA 507

Qy        377 AlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIle 396
Db        508 GCGGCAGGAGCAGCAAAGGGACTGGAGTATCTGCATGATAAAGCGAATCCGCCTGTGATC 567

Qy        397 HisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAla 416
Db        568 TACAGAGACCTGAAATCATCCAACATTCTTCTCGGTGATGGCTATCACCCAAAGTTATCT 627

Qy        417 AspPheGlyLeuAlaLysIleAlaSer---AspThrAsnThrHisValSerThrArgVal 435
Db        628 GATTTTGGGTTAGCTAAGTTAGGTCCCGTGGGCGATAAAACACATGTGTCAACTCGTGTG 687

Qy        436 MetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLys 455
Db        688 ATGGGCACATATGGTTATTGTGCACCGGAATATGCCATGACAGGGCAACTCACATTGAAA 747

Qy        456 SerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVal 475
Db        748 TCCGATGTTTATAGCTTTGGGGTTGTGTTTCTCGAGCTCATCACGGGTCGAAAAGCTATT 807
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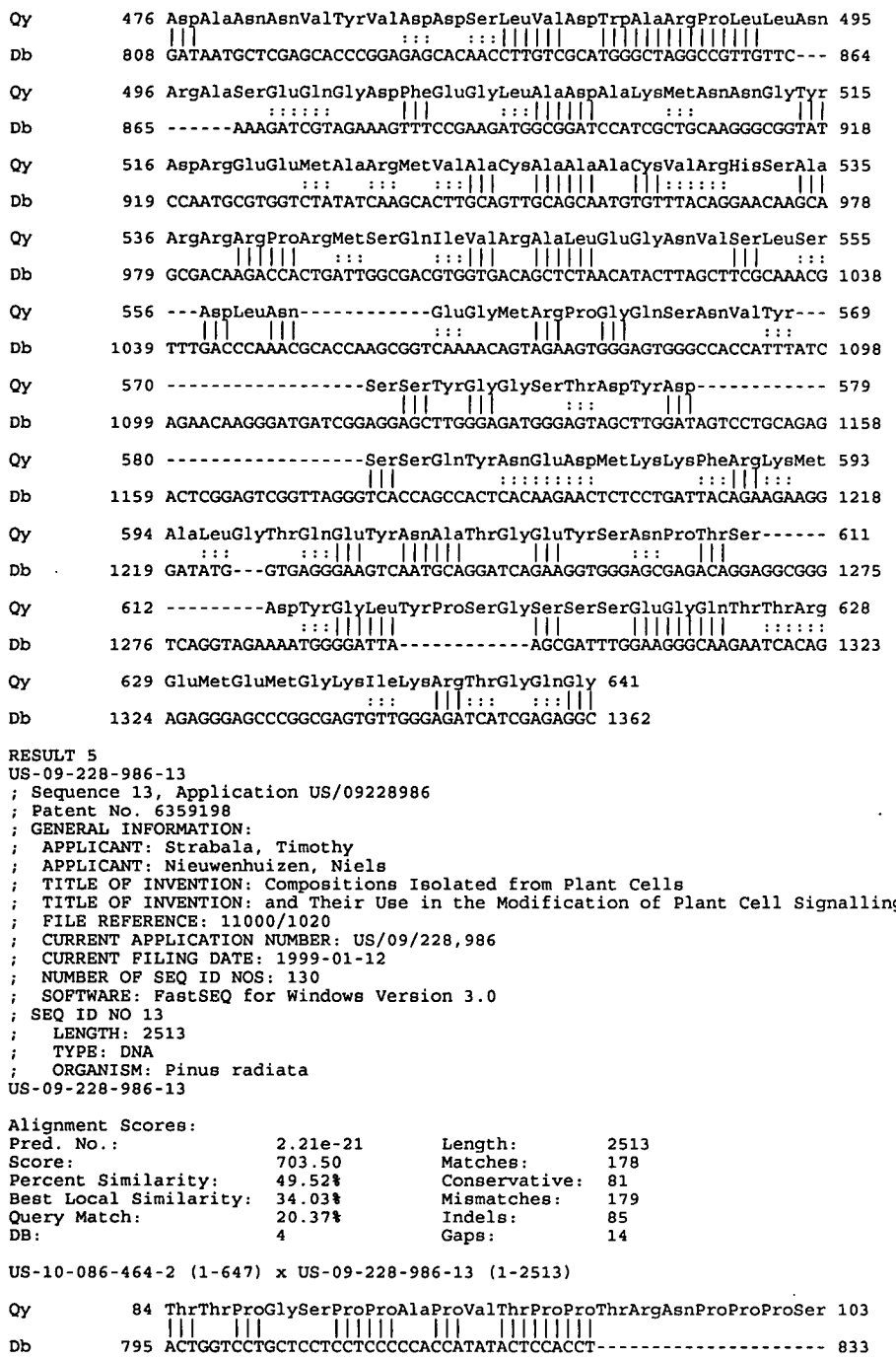
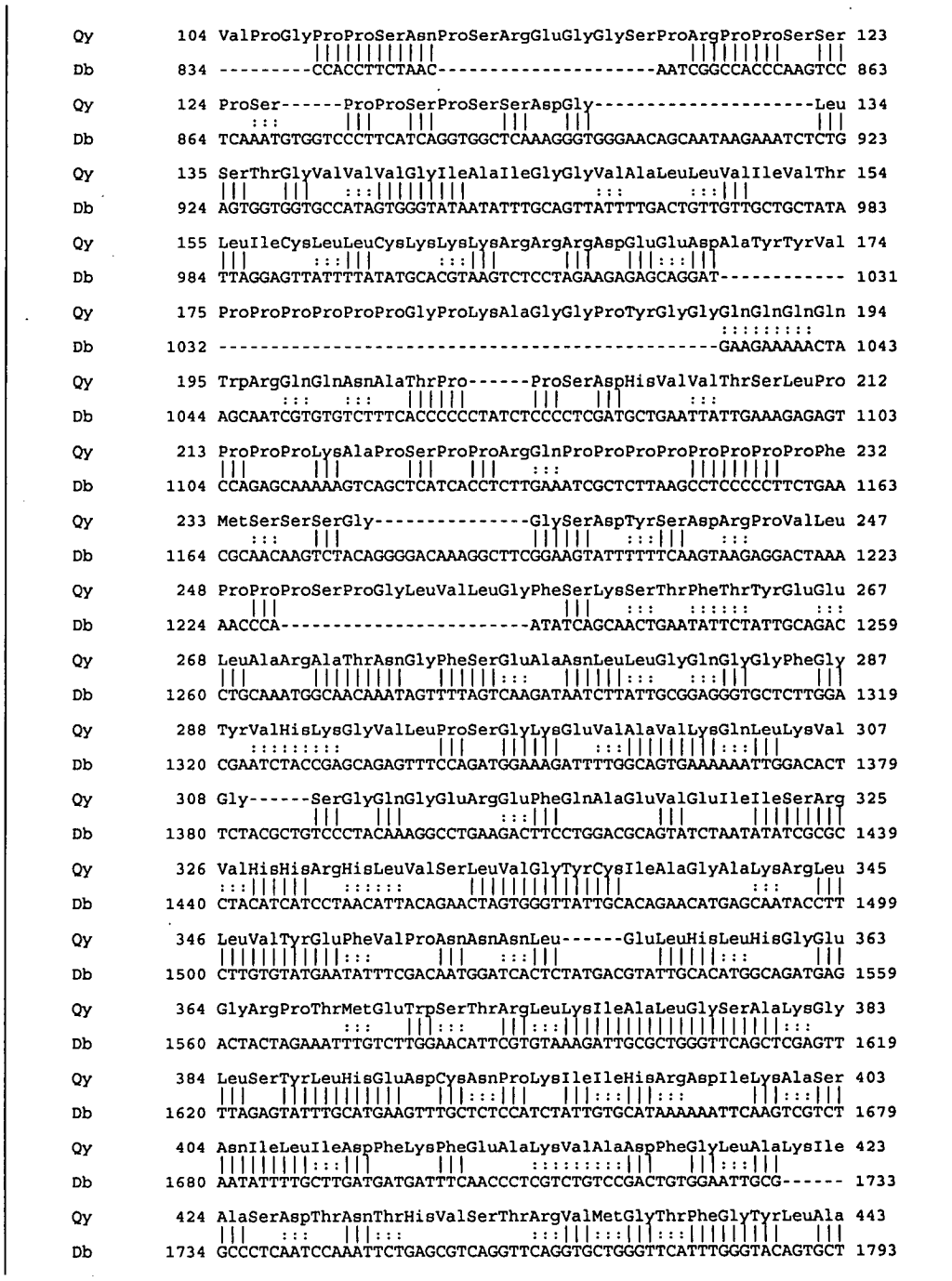


RESULT 5
US-09-228-986-13
; Sequence 13, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-13

Alignment Scores:

Pred. No.:	2.21e-21	Length:	2513
Score:	703.50	Matches:	178
Percent Similarity:	49.52%	Conservative:	81
Best Local Similarity:	34.03%	Mismatches:	179
Query Match:	20.37%	Indels:	85
DB:	4	Gaps:	14

US-10-086-464-2 (1-647) x US-09-228-986-13 (1-2513)



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Qy        444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463
              |||||||||      ||||||     |||   ||||||||||||:::||||||||||||
Db       1794 CCTGAATATGTCATGTCAGGAATCTATACAATGAAGAGCGATGTGTATAGTTTTGGAGTG 1853

Qy        464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAsp 483
              |||:::||||||||||:::|||||||||:::|||:::|||::::::             :::
Db       1854 GTAATGCTTGAGCTTTTGACAGGCCGGAAGCCCTTGGATAGTTCAAGAACAAGGTCAGAA 1913

Qy        484 AspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPhe 503
                 |||||||||   ||||||   |||   |||:::                   |||
Db       1914 CAGTCATTAGTAAGATGGGCCACCCCTCAGCTTCAT-----------------GATATT 1955

Qy        504 GluGlyLeuAla---------AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              :::   ||||||         |||     :::         |||      :::   :::
Db       1956 GATGCATTGGCAAAGATGGTTGATCCAGCTTTGAAGGGAAGTTATCCTGCAAAATCTCTC 2015

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              :::|||              |||   |||::::::                 ||||||
Db       2016 TCGCGCTTTGCTGATATTATTGCCCTCTGCATTCAGCCTGAACCAGAATTCCGTCCTCCA 2075

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||::::::|||:::||||||         :::      :::   ||||||:::
Db       2076 ATGTCTGAAGTGGTGCAAGCATTGGTTCGTATGATGCAACGGGCTAGCCTCAATAAGAGG 2135

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              |||       :::                          :::   |||:::|||
Db       2136 ATGACAGGAGATGAA-------------------------ACTGCAGACCACGATCCT 2168

Qy        581 SerGlnTyr 583
              :::   |||
Db       2169 GCAGATTAT 2177

RESULT 6
US-09-228-986-7
; Sequence 7, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2432
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-09-228-986-7

Alignment Scores:
Pred. No.:              2.44e-20      Length:         2432
Score:                  678.00        Matches:        147
Percent Similarity:     63.05%        Conservative:   68
Best Local Similarity:  43.11%        Mismatches:     104
Query Match:            19.64%        Indels:         22
DB:                     4             Gaps:           8

US-10-086-464-2 (1-647) x US-09-228-986-7 (1-2432)

Qy        254 LeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsn 273
              :::   ||||||      |||      |||::::::::::||||||      :::||||||
Db       1046 ATTTGTCTAGGGCATTTGAAG---AGATTCTCATTCAAAGAGTTACGTGTTTCCACTAAT 1102

Qy        274 GlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyVal 293
              ||||||     |||:::||||||   ||||||:::|||   |||:::||||||
Db       1103 AATTTTAGTAGCAAGAATATTTTAGGAGTAGGAGGATATGGAATTGTCTATAAAGGATTC 1162

Qy        294 LeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer---GlyGlnGly 312
              |||      |||      ||||||:::|||:::||||||   |||:::   |||   |||
Db       1163 CTACAAGATGGCACTATAGTAGCAATAAAAAGGTTGAAAGATGGTAATGTGGGAGGAGGA 1222

Qy        313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
              |||   :::||||||   |||||||||:::||||||         ||||||:::|||:::
Db       1223 GAAATTCAATTTCAAACAGAGGTGGAAATGATCAGCTTGGCTGTGCATAGGAACCTATTA 1282

Qy        333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
                 |||   |||:::|||             :::|||||||||||||||   ::::::|||
Db       1283 CGATTGTATGGATTTTGCACAACCTCCAGAGAGAGGCTTCTGGTCTATCCCTACATGCCA 1342

Qy        353 AsnAsnAsnLeuGlu------LeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              |||   ::::::         |||      |||      |||:::      ::::::|||
Db       1343 AATGGAAGTGTGGCCTCTTGTCTTAGAGATCATATTAATGGAAAGCTTGCCCTGGACTGG 1402

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
              ||||||   :::||||||||||||:::|||:::||||||   ||||||||||
Db       1403 CCTACTCGCAAGCGTATAGCCCTTGGAGCAGCTAGGGGACTGTTATATTTGCATGAGCAA 1462

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::|||||||||||||||||||:::||||||:::||||||||:::|||
Db       1463 TGTGATCCCAAGATTATTCACCGGGATGTGAAAGCAGCAAATATATTACTGGATGAATAT 1522

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              |||||||||   |||   |||||||||||||||||:::      ::::::|||
Db       1523 TTTGAAGCTGTTGTTGGAGATTTTGGGTTAGCAAAGCTCTTGGATCACAGGGATTCTCAT 1582

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              |||:::|||   |||   ||||||   |||::::::||||||||||   ::::::|||
Db       1583 GTGACTACTGCTGTTCGAGGGACGGTAGGTCACATTGCCCCAGAATACCTTTCAACGGGA 1642

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              :::   :::||||||::|||||||||   ||||||::::::||||||||||||||||||
Db       1643 CAATCTTCAGAGAAAACTGATGTATTTGGCTTTGGGATATTACTGTTGGAACTCATTACA 1702

Qy        471 GlyArgArgProValAsp-----------AlaAsnAsnValTyrValAspAspSerLeu 486
              |||:::|||   :::|||           |||          |||         :::
Db       1703 GGACAAAGGGCTTTAGATTTTGGCCAGGCTGCAAAGCAAAAAGTTGTA---------ATG 1753

Qy        487 ValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeu 506
              :::||||||   :::   |||              ::::::                |||
Db       1754 CTGGATTGGGTAAAGAAGCTT-----------CATCAAGAGAAGAAGTTGCACCTCCTT 1801

Qy        507 AlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCys 526
              ||||||      :::         :::||||||   |||:::      ||||||
Db       1802 GCTGATAAAGATCTTAAGGGCAATTTTGATAGAGTTGAGCTAGAAGAGATGGTTCAGGTT 1861

Qy        527 AlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArg 546
              :::   |||  :::                |||||:::|||      ::::::|||
Db       1862 TCTTTGCTATGCACCCAATTTCAGCCTGGACATCGTCCAAAAATGTGTGATGTTTTGAGA 1921

Qy        547 AlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSer 566
              |||||||||:::      |||::::::      |||   ::::::      ::::::
Db       1922 ATGTTGGAAGGTGAT---GGATTGACAGAACGGTGGGAAACATTGCAAAAAATTGAAACC 1978

Qy        567 AsnValTyrSer-----------------SerTyrGlyGlySerThrAspTyrAspSer 580
                 |||                      :::|||           :::   ||||||
Db       1979 CCCCGATACAGAGTAACTGAGATACCCATAACATATTCCGAGTTGGTTGAAGAAGATTCT 2038

Qy        581 Ser 581
              |||
Db       2039 TCT 2041

RESULT 7
US-09-602-472A-3
; Sequence 3, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
;  APPLICANT: Bidney, Dennis L.
;  APPLICANT:  Hu, Xu
;  APPLICANT:  Li, Guihua
;  TITLE OF INVENTION: Sunflower Disease Resistance Genes
;  FILE REFERENCE: 35718/200630
;  CURRENT APPLICATION NUMBER: US/09/602,472A
;  CURRENT FILING DATE:  2000-06-23
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;  PRIOR APPLICATION NUMBER: 60/140,876
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1559
;   TYPE: DNA
;   ORGANISM: Helianthus annuus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (81)...(1319)
US-09-602-472A-3

Alignment Scores:
Pred. No.:              4.39e-20        Length:         1559
Score:                  667.50          Matches:        165
Percent Similarity:     57.50%          Conservative:   65
Best Local Similarity:  41.25%          Mismatches:     117
Query Match:            19.33%          Indels:         57
DB:                     4               Gaps:           9

US-10-086-464-2 (1-647) x US-09-602-472A-3 (1-1559)

Qy        219 SerProProArgGlnProProProProProProProProPheMetSerSerSerGlyGly 238
              ||||||     :::|||     ||||||  ||||||
Db        131 TCACCAAAAAGTCGGCCATGAAGTCCACCCAT-CCGCCCCTT------------------ 171

Qy        239 SerAspTyrSerAspArgProValLeuProProProSerProGlyLeuVal--------- 255
                                  |||:::  |||       |||||||||:::
Db        172 ------------------CCAATATTTCCAGATTATCTTCCGGGGTTGATAGGATGAAAA 213

Qy        255 ------------------------------------------------------------ 255

Db        214 CGAGAAACAATGTTAATAATGCTGCTAGCCTAAGGAGGGAGTCATCAGGGCCGCCGGATG 273

Qy        256 LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPhe 275
              |||     :::     |||||||||:::   |||||||||  |||||||||   |||
Db        274 CTCAA-ATCGCCGCACAAACCTTCACATTCCGCGAGCTTGCAGCCGCCACCAATAATTTT 332

Qy        276 SerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu--- 294
                        |||   :::|||||||||||||   |||:::::|||   |||
Db        333 CAGCCTGATTGCTTCTTAAGGGAGGGTGGTTTTGGTTGTGTATATAGAGGACGTCTTCAG 392

Qy        295 ProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArg 314
                ||||||:::   |||||||||||||||||                |||||   |||
Db        393 AGTAGTGGTCAAGTTGTAGCTGTTAAACAGCTGGATAGAAATGGACTCCAAGGTAACCGT 452

Qy        315 GluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeu 334
              ||||||     ||||||   :::::::|||   :::||||||   :::|||||||:|||
Db        453 GAGTTTCTTGTTGAAGTTCTTATGCTCAGCCTTTTACATCATCCAAACTTGGTCAATTTG 512

Qy        335 ValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 354
              :::||||||||||      |||   :::|||||||||||||||||||||:::
Db        513 ATTGGCTACTGCGCTGACGGTGACCAACGACTTCTTGTCTATGAGTTTATGGCCTTGGGT 572

Qy        355 AsnLeuGluLeuHisLeuHisGly------GluGlyArgProThrMetGluTrpSerThr 372
              :::||||||   |||||||||                  |||      ::::::|||   |||
Db        573 TCCTTGGAAGATCACCTTCATGATGTTCCGCCTGACAGAGAACCATTAGATTGG---ACA 629

Qy        373 -ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAs 392
               |||:::|||||||||      :::||||||||||||   :::||||||:::       ||
Db        630 CAGGATGAAGATAGCGGCTGT-GCAGCCAAGGGGTTGGAGTTTCTTCATGATAAAGCTAA 688

Qy        392 nProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGl 412
              ||||   :::|||:::||||||   |||:::||||||||||||:::|||      |||::
Db        689 CCCACCAGTTATTTATCGGGACTTCAAATCATCAAACATTTTGCTGGATGAGGGATTTCA 748

Qy        412 uAlaLysValAlaAspPheGlyLeuAlaLysIleAla---SerAspThrAsnThrHisVa 431
              :   |||::::::|||||||||||||||||:::      :::          :::|||||
Db        749 ACCAAAGCTGTCCGACTTCGGGCTCGCGAAACTGGGCCCCACTGGAGACAAGTCTCATGT 808

Qy        431 lSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLy 451
              |||||||||||||||||||||:::||||||   ||||||||||||||   :::|||::
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Db        809 TTCCACACGGGTGATGGGTACATACGGTTACTGTGCTCCTGAGTATGCCATGACTGGTCA 868

Qy        451 sLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGl 471
              :||||||   ||||||||||||:::|||||||||||||||   ||||||||||||||||
Db        869 GTTAACGGTCAAATCCGATGTGTACAGCTTTGGTGTCGTCTTTTTAGAGCTTATTACCGG 928

Qy        471 yArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaAr 491
              ||||:::   :::|||:::         :::         :::||||||   ||||||||
Db        929 TAGAAAAGCCATAGATAGCACTCAACCACATGGACAGCAGAACCTGGTGACATGGGCACG 988

Qy        491 gProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMe 511
              |||||||   |||         ::::::      |||      |||   |||   :::::
Db        989 ACCTTTGTTCAAC---------GACAGAAGGAAATTCACATCGTTGGTGGACCCACGGTT 1039

Qy        511 tAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVa 531
              :         |||           :::   :::   :::|||   |||:::   |||::
Db       1040 AGAAGGTCGGTACCCAATGCGGGGGCTGTACCAGGCGCTAGCGGTGGCATCCATGTGTAT 1099

Qy        531 lArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAs 551
              ::::                |||||   ::::::   :::|||   ||||||
Db   .    1100 TCAAGAACAGGTTGCAGCCCGGCCTTTGATTGCTGACGTGGTAACTGCGCTATCTTATCT 1159

Qy        551 nValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSer------------As 567
                              |||:::|||      |||      |||              ||
Db       1160 TGCA--------------AACCAGGGGTACGATCCGAC-CACAGCTCCCAGCTTCATAA 1203

Qy        567 nValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAsp 586
              |:::   ||||||   ||||||                  ::::::::::::::::::::
Db       1204 CATCATCAGCAGCGCCGGCGGCAAGGAGAGACTTAAAACCGCAAGGTTTTCGAAAAAC 1261

RESULT 8
US-08-881-706-1
; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
;  APPLICANT: Chong, Joane
;  APPLICANT: Li, Jianming
;  TITLE OF INVENTION: Receptor Kinase BIN1
;  FILE REFERENCE: 07251/022001
;  CURRENT APPLICATION NUMBER: US/08/881,706
;  CURRENT FILING DATE: 1997-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4104
;   TYPE: DNA
;   ORGANISM: Arabidopsis sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(3687)
US-08-881-706-1

Alignment Scores:
Pred. No.:              4.4e-17         Length:         4104
Score:                  604.50          Matches:        161
Percent Similarity:     47.21%          Conservative:   84
Best Local Similarity:  31.02%          Mismatches:     148
Query Match:            17.51%          Indels:         127
DB:                     3               Gaps:           14

US-10-086-464-2 (1-647) x US-08-881-706-1 (1-4104)

Qy        107 ProPro------------SerAsnProSerArgGluGlyGlySerProArgProProSer 122
              ||||||           :::||||||          |||   |||   |||
Db       2350 CCACCGGCTAAGTTCTTGAACAATCCTGGTCTC---TGTGGTTATCCTCTTCCGCGGTGT 2406

Qy        123 SerProSerProProSerProSerSerAspGlyLeu--------------SerThrGly 137
                ||||||            ::::::||||||                 |||   |||
Db       2407 GATCCTTCA------------AATGCAGACGGTTATGCTCATCATCAGAGATCTCATGGA 2454

Qy        138 ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCys 157
                                  |||  ||||||:::   ::::::   :::   :::|||
Db       2455 AGGAGACCAGCGTCCCTTGCTGGTAGTGTGGCGATGGGATTGTTGTTCTCTTTTGTGTGT 2514
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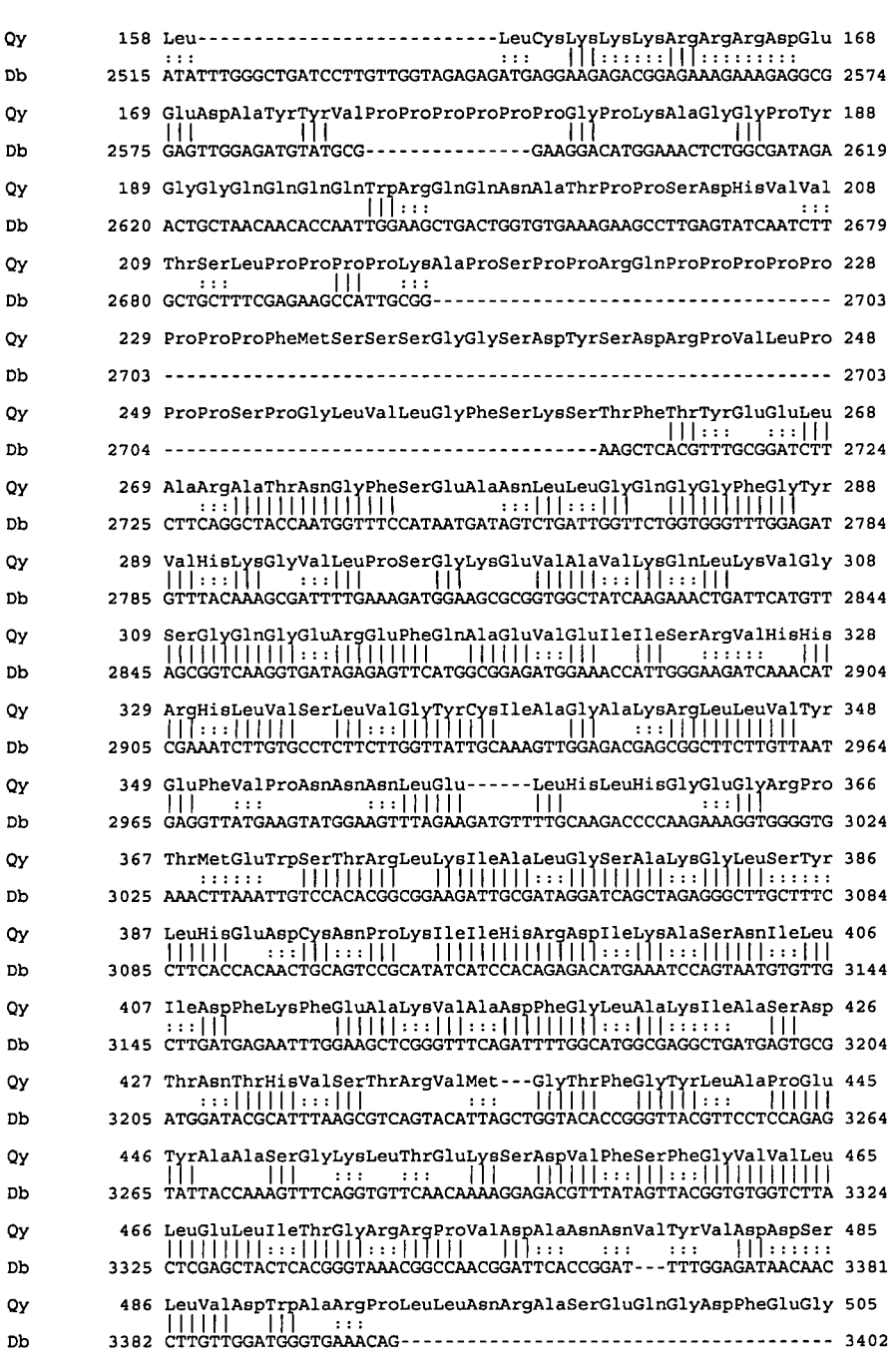

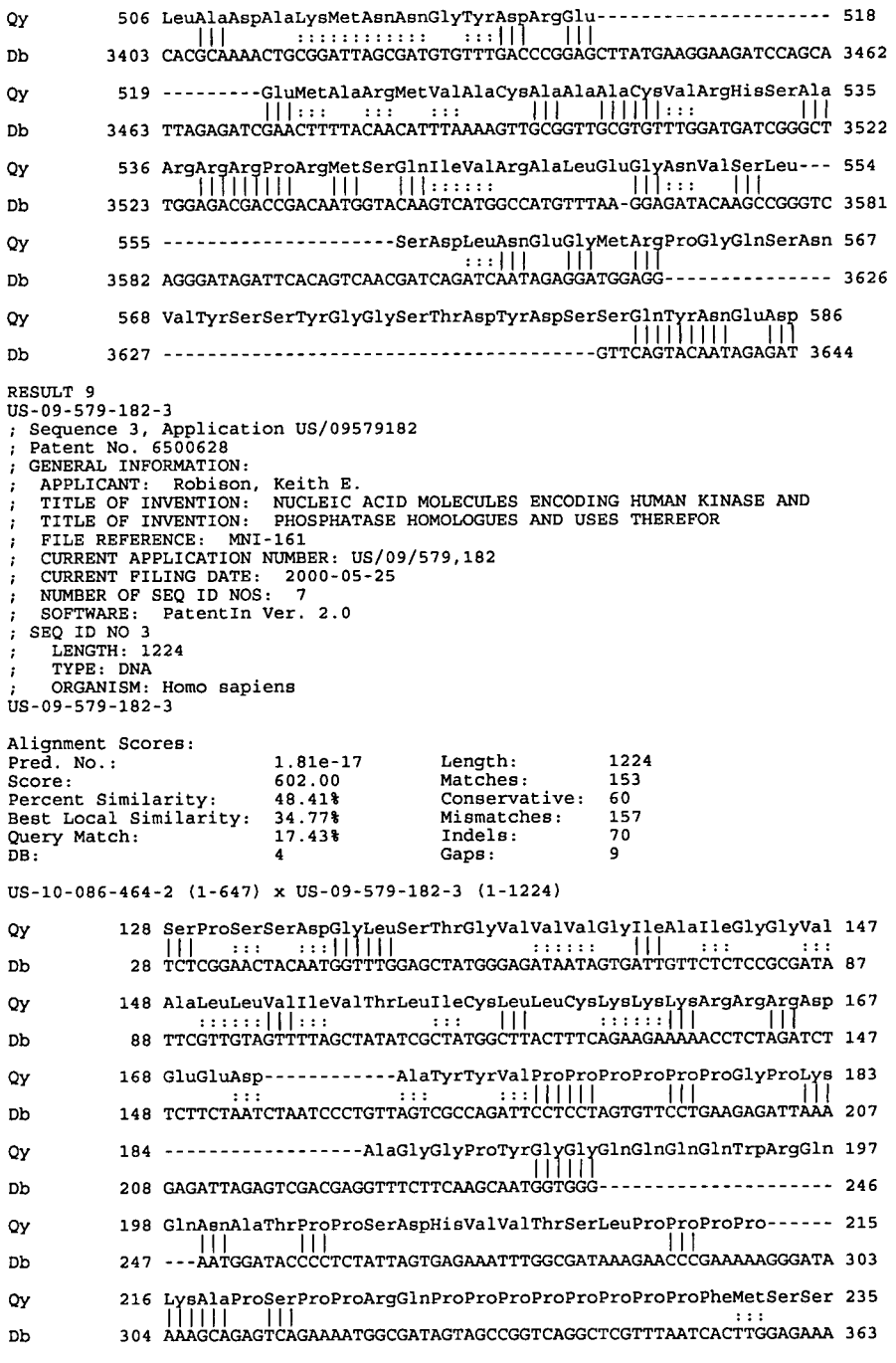

RESULT 9
US-09-579-182-3
; Sequence 3, Application US/09579182
; Patent No. 6500628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-3

Alignment Scores:

Pred. No.:	1.81e-17	Length:	1224
Score:	602.00	Matches:	153
Percent Similarity:	48.41%	Conservative:	60
Best Local Similarity:	34.77%	Mismatches:	157
Query Match:	17.43%	Indels:	70
DB:	4	Gaps:	9

US-10-086-464-2 (1-647) x US-09-579-182-3 (1-1224)

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Qy        236 SerGlySerAspTyrSerAspArgProValLeuProProProSerPro------Gly 253
Db        364 AAAGACGGATCGAGCGTATCTTCTGCTAATCCTTTGACAGCTCCATCTCCTTTGTCTGGT 423

Qy        254 LeuVal-----------LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla 269
Db        424 CTTCCTGAGTTTTCTCACCTTGGATGGGGA---CATTGGTTCACTCTTAGAGATCTTCAG 480

Qy        270 ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrVal 289
Db        481 ATGGCTACTAATCAGTTTTCAAGGGATAATATCATCGGTGATGGTGGATATGGAGTTGTT 540

Qy        290 HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer 309
Db        541 TACCGCGGTAACCTTGTTAATGGTACTCCTGTTGCTGTTAAAAAGTTGCTCAACAATTTA 600

Qy        310 GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg 329
Db        601 GGACAAGCTGATAAAGACTTCAGAGTTGAAGTTGAAGCTATAGGTCACGTTCGACATAAA 660

Qy        330 HisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGlu 349
Db        661 AACTTGGTCCGCCTTCTCGGATATTGTATGGAAGGAACGCAGAGG--------------- 705

Qy        350 PheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGlu 369
Db        705 ------------------------------------------------------------ 705

Qy        370 TrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGlu 389
Db        706 ----------------------------------------CTCGCGTACCTTCACGAG 723

Qy        390 AspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPhe 409
Db        724 GCGATTGAGCCAAAAGTGGTGCACAGAGACATTAAGTCTAGTAACATTCTGATTGATGAC 783

Qy        410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThr 429
Db        784 AAATTCAATTCTAAAATTTCTGACTTTGGACTTGCTAAACTACTTGGTGCTGATAAGAGT 843

Qy        430 HisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSer 449
Db        844 TTTATAACTACTAGAGTTATGGGTACCTTCGGTTACGTAGCTCCAGAGTATGCGAATTCC 903

Qy        450 GlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIle 469
Db        904 GGTCTTCTGAATGAGAAAAGCGATGTCTACAGCTTCGGGGTTGTACTCTTGGAAGCTATA 963

Qy        470 ThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp 489
Db        964 ACTGGTAGATATCCGGTAGACTATGCTCGTCCACCACCCGAGGTACATTTGGTGGAGTGG 1023

Qy        490 AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAla 509
Db       1024 CTGAAGATGATGGTC-----------CAACAAAGACGATCAGAAGAAGTGGTTGATCCA 1071

Qy        510 LysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAla 529
Db       1072 AACCTTGAAACAAAACCATCTACAAGTGCTTTGAAAAGAACACTATTGACTGCTTTGAGA 1131

Qy        530 CysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGlu 549
Db       1132 TGTGTTGATCCAATGTCTGAGAAAAGACCGAGGATGAGCCAAGTTGCACGTATGCTTGAA 1191
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RESULT 10
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-11

Alignment Scores:

Pred. No.:	4.95e-17	Length:	3097
Score:	600.50	Matches:	173
Percent Similarity:	46.08%	Conservative:	80
Best Local Similarity:	31.51%	Mismatches:	172
Query Match:	17.39%	Indels:	126
DB:	4	Gaps:	13

US-10-086-464-2 (1-647) x US-09-228-986-11 (1-3097)

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Qy         66 ProSerThrProGlySerProProPro--------------------------LeuPro 76
Db       1523 CCTGCAAGTTCTGGACGTCCAAAACAACAGCTTAGACGGAGTTGTTCCCGACGGCTTGGG 1582

Qy         77 GlnProSerProProAlaProThrThrProGlySerProProAlaProValThrPro--- 95
Db       1583 AGAGCTGAAAGACCTTCACCTACTGGACTTGGAGAATAACCTGCTACAAG-GTACCTTAC 1641

Qy         96 ----------------------ProThrArgAsnProProProSerValProGlyProPro 108
Db       1642 CAGATTCCTTGAACAGACAGAGCTTGGAGGTCAGAACCTCAGGAAACTTGTGTCTTTCCT 1701

Qy        109 SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerPro------ 126
Db       1702 TCTCCACAACCGCGTGC-GGTGATGCATCATCTAGTCCTTCAATTGAGGCACCGCAAGTT 1760

Qy        127 ---------ProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAla 143
Db       1761 ACAATAGTTCCCGAGAGAAACAAAGGGGGACATAATCGTTTAGCCATTATACTCGGAGCA 1820

Qy        144 IleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLys 163
Db       1821 GTCGGAGGAGTATCACTAGCTATTTTACTCATCCCGCTCTTCGTATTCATGTACAGAAGG 1880

Qy        164 ArgArgArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLys 183
Db       1881 AGAGGAAGAACTGAA------------------------------------------- 1895

Qy        184 AlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProPro 203
Db       1895 ------------------------------------------------------------ 1895

Qy        204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223
Db       1895 ------------------------------------------------------------ 1895

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
Db       1896 ----------------------------------------ATGTCATATACGGAA 1910

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
Db       1911 AGGGCAGTCGCAGACGTGAGAAACTGGAAT--------------GCAGCTAAGATTTTT 1955

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
Db       1956 TCCTACAAAGAGATCAAAACAGCTACAAACAACTTTAAAGAA------GTCATTGGTCAT 2009

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
Db       2010 GGAAGTTTTGGATCCGTGTACCTGGGAAACCTTCCAGTTGGAAAACTAGTTGCTGTGAAA 2069
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Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
                      :::     |||         |||      ||||||   ::::::
Db       2070 GTGCGGTTTGATAAAACCCAACTTGGTGCAGATTCTTTCATAAATGAGGTTCGTCTCTTA 2129

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
              |||:::|||   |||::::::||||||||||||   |||:::|||             :::
Db       2130 TCACAAGTCCGCCATCAGAACCTTGTCAGTCTGGAAGGATTTTGTTATGAGTCGCAGCGT 2189

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGlu 363
              ::::::||||||||||||::::::|||      :::|||          |||:::|||
Db       2190 CAGATTTTAGTCTATGAATATCTACCGGGTGGATCACTGGCTGATCAACTGTATGGTCCA 2249

Qy        364 Gly------ArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
                  :::   ::::::   |||      ||||||||||||||:::   :::|||
Db       2250 AACAGTAGGAAATTCTCACTAAGCTGGGTTCGTAGACTCAAGATTGCTGTTGATGCTGCA 2309

Qy        382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
              |||||||||   |||||||||         ||||||:::||||||||||||||||||||
Db       2310 AAAGGACTGGACTATCTACATAATGGAAGCAATCCTCGAATCATACACCGAGACATCAAG 2369

Qy        402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
                |||||||||||:::|||   :::      |||::::::   ||||||||||||:::
Db       2370 TGCAGTAATATACTATTGGACAAGGAGATGAATGCAAGACTTTGCGACTTTGGGCTCTCT 2429

Qy        422 Lys------IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              |||      |||      |||      |||||||||:::|||   |||   ||||||
Db       2430 AAGCAAATGATCCAGCCAGACGCA---ACTCACGTGACCACTGTCGTCAAGGGCACAGCT 2486

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
              |||||||||   |||||||||   ::::::   :::||||||||||||||||||||:::
Db       2487 GGTTACCTCGACCCTGAATATTACTCCACCCAACAACTTACAGAGAAAAGCGACGTCTAT 2546

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
              |||||||||||||||||||||||||||   ||||||   |||::::::   :::
Db       2547 AGCTTTGGAGTTGTGCTTTTGGAGCTCATCTGTGGACGAGAGCCGTTAAATCATTCAGGA 2606

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
                      :::|||||||   ||||||:::|||   |||             :::
Db       2607 ACTCCAGATTCCTTCAATTTGGTTTTATGGGCAAAGCCCTACTTG-----------CAG 2654

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
              |||   ||||||   :::   |||      :::          :::|||   |||
Db       2655 GCAGGTGCATTTGAG---ATAGTGGATGAGAGTTTAGGGGGAAGTTTCGATGTGGAAAGC 2711

Qy        520 MetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPro 539
              |||   ::::::         |||         |||         |||      ||||||
Db       2712 ATGAGGAAAGTGGCAAAAATCGCTGTGAGGTCTGTAGAGAGGGATGCATCACTAAGGCCA 2771

Qy        540 ArgMetSerGlnIleValArgAlaLeuGluGly------AsnValSerLeuSerAspLeu 557
                 ::::::||||||:::      |||:::      ::::::   ||||||
Db       2772 ACCATTGCACAGATACTGTCTGTGCTCAAAGAGGCTTACAGCATTCAGCTCTCT------ 2825

Qy        558 AsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAsp 577
                                                |||   :::      |||      :::
Db       2826 --------------------------------TATCTTGCAGCCTCTGGACATGTGAAC 2852

Qy        578 TyrAspSerSerGlnTyrAsnGluAsp 586
                    |||   ||||||:::|||
Db       2853 TGAATCTACTCGTATTACAACCAAGAC 2879

RESULT 11
US-08-587-889-1
; Sequence 1, Application US/08587889
; Patent No. 5654397
;  GENERAL INFORMATION:
;    APPLICANT:  CAO, Zhaodan
;    APPLICANT:  CROSTON, Glenn E.
;    APPLICANT:  GOEDDEL, David V.
;    TITLE OF INVENTION:  INTERLEUKIN-1 RECEPTOR-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN KINASE AND BINDING ASSAY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/587,889
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Osman Ph.D., Richard Aron
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  A-60916
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 494-8700
;      TELEFAX:  (415) 494-8771
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3590 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-587-889-1

Alignment Scores:
Pred. No.:                3.48e-16        Length:          3590
Score:                    581.50          Matches:         208
Percent Similarity:       38.68%          Conservative:    86
Best Local Similarity:    27.37%          Mismatches:      239
Query Match:              16.84%          Indels:          229
DB:                       1               Gaps:            28

US-10-086-464-2 (1-647) x US-08-587-889-1 (1-3590)

Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
              |||:::      |||   ||| |||:::      ||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla------------------------ProProPr 32
              |      |||         :::|||                             |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro---------------------------------------- 39
              ||||      ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                  |||   |||      |||   |||      |||   |||   :::||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro------------------------------ThrProSerTh 68
              |||                                               |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
              ||||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
              |||   |||   :::   ||||||          |||   |||      ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519
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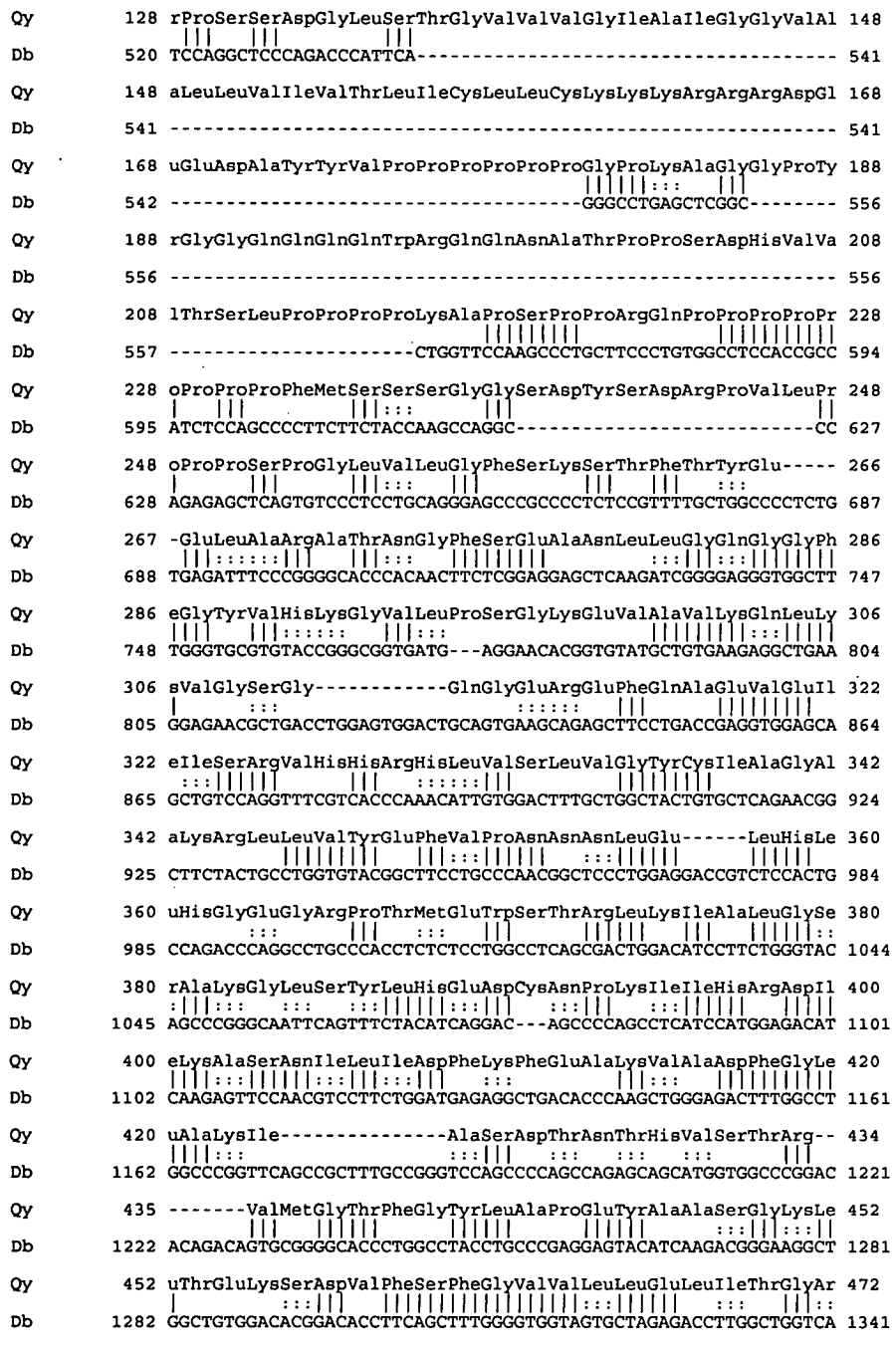

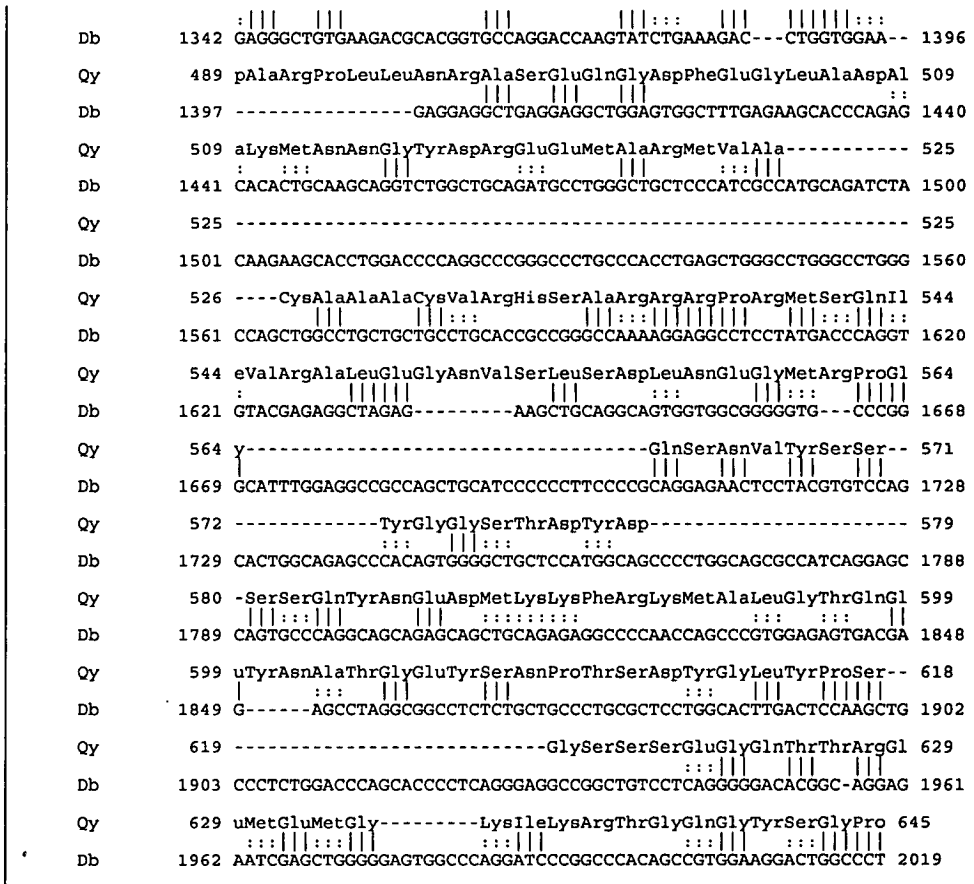

RESULT 12
US-09-016-434-1093
; Sequence 1093, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1093:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3590 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1220312
US-09-016-434-1093

Alignment Scores:
Pred. No.:                3.48e-16      Length:          3590
Score:                    581.50        Matches:         208
Percent Similarity:       38.68%        Conservative:    86
Best Local Similarity:    27.37%        Mismatches:      239
Query Match:              16.84%        Indels:          229
DB:                       4             Gaps:            28

US-10-086-464-2 (1-647) x US-09-016-434-1093 (1-3590)

Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
              |||:::      |||   ||| |||:::      |||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla------------------------ProProPr 32
              |       |||          :::|||                              |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro----------------------------------- 39
              ||||     ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                  |||   |||      |||   |||      |||   |||   :::||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro------------------------------ThrProSerTh 68
              |||                                                |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
              ||||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
              |||   |||   :::   ||||||         |||   |||      ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148
              |||   |||         |||
Db        520 TCCAGGCTCCCAGACCCATTCA---------------------------------- 541

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db        541 ------------------------------------------------------------ 541

Qy        168 uGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTy 188

                                                  ||||||:::   |||
Db        542 ----------------------------------GGGCCTGAGCTCGGC-------- 556

Qy        188 rGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValVa 208

Db        556 ------------------------------------------------------------ 556

Qy        208 lThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPr 228
                                          |||||||||          ||||||||||
Db        557 ---------------------CTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCC 594

Qy        228 oProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuPr 248
              |   |||         |||:::      |||                            ||
Db        595 ATCTCCAGCCCCTTCTTCTACCAAGCCAGGC-------------------------CC 627

Qy        248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu----- 266
              |      |||      |||:::   |||         |||   |||   :::
Db        628 AGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTCTCCGTTTTGCTGGCCCCTCTG 687

Qy        267 -GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPh 286
               |||::::::|||   |||:::   ||||||||        :::|||:::||||||||
Db        688 TGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAGGGTGGCTT 747

Qy        286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306
              ||||   |||::::::   ||:::                    |||||||||:::|||||
Db        748 TGGGTGCGTGTACCGGGCGGTGATG---AGGAACACGGTGTATGCTGTGAAGAGGCTGAA 804

Qy        306 sValGlySerGly------------GlnGlyGluArgGluPheGlnAlaGluValGluIl 322
              |      :::                  ::::::   |||      |||||||||
Db        805 GGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTGGAGCA 864

Qy        322 eIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342
              :::||||||      |||   ::::::|||      |||||||||
Db        865 GCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAGAACGG 924

Qy        342 aLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLe 360
                  |||||||||   |||:::||||||   :::||||||      ||||||
Db        925 CTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTCCACTG 984

Qy        360 uHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380
                  :::      |||   :::   |||      ||||||   |||   ||||||::
Db        985 CCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTGGGTAC 1044

Qy        380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIl 400
              :|||:::   :::   :::||||||:::|||   :::|||   :::||||||   |||||
Db       1045 AGCCCGGGCAATTCAGTTTCTACATCAGGAC---AGCCCCAGCCTCATCCATGGAGACAT 1101

Qy        400 eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420
              ||||:::||||||:::|||:::|||   :::          |||:::   ||||||||||
Db       1102 CAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGCCT 1161

Qy        420 uAlaLysIle---------------AlaSerAspThrAsnThrHisValSerThrArg-- 434
              ||||:::                 :::|||   :::   :::   :::      |||
Db       1162 GGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGGAC 1221

Qy        435 -------ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452
                     |||   ||||||      ||||||      ||||||      :::|||:::||
Db       1222 ACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGGCT 1281

Qy        452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472
              |         :::|||   |||||||||||||||||:::||||||   :::   |||::
Db       1282 GGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGTCA 1341

Qy        472 gArgProVal---------AspAlaAsnAsnValTyrValAspAspSerLeuValAspTr 489
              :|||   |||         |||   |||:::   |||   ||||||:::
Db       1342 GAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGAC---CTGGTGGAA-- 1396

Qy        489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509
                                  |||   |||   |||                    ::
Db       1397 ---------------GAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAG 1440

Qy        509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAla----------- 525
              :   :::      |||         :::      |||      :::|||
```

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Db       1441 CACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTA 1500

Qy        525 ------------------------------------------------------------ 525

Db       1501 CAAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGG 1560

Qy        526 ----CysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544
                   |||      |||:::         |||:::|||||||||   |||:::|||:: 
Db       1561 CCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGT 1620

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564
               :      ||||||            |||      :::      |||:::  |||||
Db       1621 GTACGAGAGGCTAGAG---------AAGCTGCAGGCAGTGGTGGCGGGGGTG---CCCGG 1668

Qy        564 y-----------------------------------GlnSerAsnValTyrSerSer-- 571
                                                  |||  |||  |||  |||
Db       1669 GCATTTGGAGGCCGCCAGCTGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAG 1728

Qy        572 ------------TyrGlyGlySerThrAspTyrAsp---------------------- 579
                         :::  |||:::      :::
Db       1729 CACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGC 1788

Qy        580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGl 599
                |||:::|||      |||  :::::::::              :::  :::   ||
Db       1789 CAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGA 1848

Qy        599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618
               |      :::   |||      |||             :::   |||   ||||||
Db       1849 G------AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG 1902

Qy        619 ---------------------------GlySerSerSerGluGlyGlnThrThrArgGl 629
                                          :::|||  |||   |||
Db       1903 CCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGC-AGGAG 1961

Qy        629 uMetGluMetGly---------LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645
               :::|||:::|||         :::|||          :::|||   :::||||||
Db       1962 AATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCT 2019

RESULT 13
PCT-US96-09193-1
; Sequence 1, Application PC/TUS9609193
;  GENERAL INFORMATION:
;    APPLICANT:  Tularik, Inc.
;    TITLE OF INVENTION:  INTERLEUKIN-1 RECEPTOR-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN KINASE AND BINDING ASSAY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09193
;      FILING DATE:  JUNE 5 1996
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. Serial No. 08/587,889
;      FILING DATE:  JAN 16 1996
;      CLASSIFICATION:
;      APPLICATION NUMBER:  U.S. Serial No. 08/494,006
;      FILING DATE:  JUNE 23 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David J. Brezner
;      REGISTRATION NUMBER:  24,774
;      REFERENCE/DOCKET NUMBER:  FP-62191-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 494-8700
;      TELEFAX:  (415) 494-8771
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3590 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US96-09193-1

Alignment Scores:
Pred. No.:                3.48e-16      Length:          3590
Score:                    581.50        Matches:         208
Percent Similarity:       38.68%        Conservative:    86
Best Local Similarity:    27.37%        Mismatches:      239
Query Match:              16.84%        Indels:          229
DB:                       5             Gaps:            28

US-10-086-464-2 (1-647) x PCT-US96-09193-1 (1-3590)

Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
                ||:::      |||   ||| |||:::      ||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla-----------------------ProProPr 32
                |          |||          :::|||                          |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro---------------------------------------- 39
                ||||      ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                  |||   |||      |||   |||      |||   |||   :::||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro-----------------------------ThrProSerTh 68
                |||                                           |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
                |||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
                |||   |||   :::   ||||||         |||   |||      ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148
                |||   |||         |||
Db        520 TCCAGGCTCCCAGACCCATTCA---------------------------------------- 541

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db        541 ------------------------------------------------------------ 541

Qy        168 uGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTy 188
                                                  ||||||:::   |||
Db        542 ----------------------------------GGGCCTGAGCTCGGC-------- 556

Qy        188 rGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValVa 208

Db        556 ------------------------------------------------------------ 556

Qy        208 lThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPr 228
                                          |||||||||           ||||||||||||
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Db        557 ----------------------CTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCC 594

Qy        228 oProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuPr 248

Db        595 ATCTCCAGCCCCTTCTTCTACCAAGCCAGGC--------------------------CC 627

Qy        248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu----- 266

Db        628 AGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTCTCCGTTTTGCTGGCCCCTCTG 687

Qy        267 -GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPh 286

Db        688 TGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAGGGTGGCTT 747

Qy        286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306

Db        748 TGGGTGCGTGTACCGGGCGGTGATG---AGGAACACGGTGTATGCTGTGAAGAGGCTGAA 804

Qy        306 sValGlySerGly------------GlnGlyGluArgGluPheGlnAlaGluValGluIl 322

Db        805 GGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTGGAGCA 864

Qy        322 eIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342

Db        865 GCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAGAACGG 924

Qy        342 aLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLe 360

Db        925 CTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTCCACTG 984

Qy        360 uHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380

Db        985 CCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTGGGTAC 1044

Qy        380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIl 400

Db       1045 AGCCCGGGCAATTCAGTTTCTACATCAGGAC---AGCCCCAGCCTCATCCATGGAGACAT 1101

Qy        400 eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420

Db       1102 CAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGCCT 1161

Qy        420 uAlaLysIle---------------AlaSerAspThrAsnThrHisValSerThrArg-- 434

Db       1162 GGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGGAC 1221

Qy        435 -------ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452

Db       1222 ACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGGCT 1281

Qy        452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472

Db       1282 GGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGTCA 1341

Qy        472 gArgProVal---------AspAlaAsnAsnValTyrValAspAspSerLeuValAspTr 489

Db       1342 GAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGAC---CTGGTGGAA-- 1396

Qy        489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509

Db       1397 ----------------GAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAG 1440

Qy        509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAla----------- 525

Db       1441 CACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTA 1500

Qy        525 ------------------------------------------------------------ 525

Db       1501 CAAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGG 1560

Qy        526 ----CysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544

Db       1561 CCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGT 1620

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564

Db       1621 GTACGAGAGGCTAGAG---------AAGCTGCAGGCAGTGGTGGCGGGGGTG---CCCGG 1668

Qy        564 y-----------------------------------GlnSerAsnValTyrSerSer-- 571

Db       1669 GCATTTGGAGGCCGCCAGCTGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAG 1728

Qy        572 ------------TyrGlyGlySerThrAspTyrAsp---------------------- 579

Db       1729 CACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGC 1788

Qy        580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGl 599

Db       1789 CAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGA 1848

Qy        599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618

Db       1849 G------AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG 1902

Qy        619 ----------------------------GlySerSerSerGluGlyGlnThrThrArgGl 629

Db       1903 CCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGC-AGGAG 1961

Qy        629 uMetGluMetGly---------LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645

Db       1962 AATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCT 2019
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RESULT 14
US-09-602-472A-5
; Sequence 5, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2114)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1475
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1475
; OTHER INFORMATION: n = A,T,C or G
US-09-602-472A-5

Alignment Scores:

Pred. No.:	2.96e-16	Length:	2114
Score:	578.00	Matches:	143
Percent Similarity:	55.07%	Conservative:	85
Best Local Similarity:	34.54%	Mismatches:	136
Query Match:	16.74%	Indels:	51
DB:	4	Gaps:	15

US-10-086-464-2 (1-647) x US-09-602-472A-5 (1-2114)

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Qy        235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeu 254
              :::          |||   ||||||   :::|||
Db         52 GCTGAATCTTCCTCCTCATATTCACCACAACCGTGC---------------------- 87

Qy        255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
                                  ||||||:::   |||:::      ||||||
Db         88 ------------------CGTCAATTTACCTTTTCGGAGATTCAACTTGCAACCCAAAAC 129

Qy        275 PheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294
              |||   |||:::   ::::::|||:::||||||||||||   |||::::::|||
Db        130 TTTGATGAGTCGTTGGTGATAGGACGTGGGGGGTTTGGCAAGGTTTACAGAGGAACCTTC 189

Qy        295 ProSerGlyLys---------GluValAlaValLysGlnLeuLysValGlySerGlyGln 311
                 |||:::          :::   |||:::|||:::|||:::   ||||||   |||
Db        190 ACTTATGGGGAAACATACTTGGATGCTGCAATTAAGCGACTGGAATCAGGTTCTAGTCAA 249

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331
              |||       ||||||:::||||||:::|||::::::|||   :::   |||   ||||||
Db        250 GGAGCGGTAGAGTTTAGGGCTGAAATTGAGATGCTCTCAAATCTAAGGCACTGTCATTTG 309

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351
              |||||||||:::|||||||||      |||   :::   :::||||||||||||   :::
Db        310 GTGTCTTTAATTGGTTACTGTAGTGATGGGCAAGAGATGGTTCTTGTATATGAACATATG 369

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371
              ||||||      |||           ||||||   :::   |||       :::   |||
Db        370 CCCAATGGAACTCTTGCAGATCGTCTCCAC---AAGCGTCGAGCTCCTCTAACTTGGGTA 426

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis------Glu 389
                 ||||||||||||   :::|||:::|||:::||||||   |||||||||
Db        427 AGAAGACTCAAAATATGCATAGGGGCCGCTCGTGGTTTAGATTACTTGCACACTGGTACG 486

Qy        390 AspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPhe 409
                 |||      :::|||||||||||||:::|||:::::::|||||||||:::|||
Db        487 GGTATTAACCATGGAGTTATACATCGGGATGTTAAGAGCACAAATATATTGTTAGATGAC 546

Qy        410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle------AlaSerAspThr 427
                 :::   ||||||||||:::|||||||||||||:::||||||         :::
Db        547 AATTGGGCAGCTAAGGTTTCTGACTTTGGTTTGTCCAAAATTGGTCCAACAAATCAGCCT 606

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
              :::|||:::|||:::|||   |||   |||||||||||||||:::   |||:::|||
Db        607 TCAACTTATGTTAACACTTTGGTGAGAGGCACCTTTGGATATATGGATCCAGATTACTTT 666

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
              :::|||:::||||||   ||||||||||||:::::::||||||||||||||   |||
Db        667 CAAACAGGTAGGCTGACTCGAAAGTCTGACGTGTATGCCTTTGGGGTGGTCCTGTTTGAA 726

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
              ::::::   |||::::::   |||          :::   :::               |||
Db        727 GTCCTATGTGGGAAACAAGTAGTACTGATGAGGAGCAC-TGG---------GGTTTGGCA 776

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
                 ||||||:::       |||             ::::::|||      :::   :::
Db        777 ACATGGGCTCAAGACTCTCTT-----------AAAGAAGGAAGGCTAAAGCAAATTGTT 824

Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
              |||:::   :::                  :::   :::                  |||
Db        825 GATTCTAATTTAAGGGGGAGAATATCCCCAAAATGTTTGAAGGAGTTTGCACTACTAGCT 884

Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
                 |||:::            ::::::||||||   |||:::::::|||
Db        885 GACCGGTGTTTGCATAGCCGTCCCAAGCAACGTCCTGCAATGGCGGAGGTTGTGATTGGT 944

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly-----------------Met 561
              ||||||      :::::::|||   :::      |||                   :::
Db        945 CTTGAGTCAATCCTAGCCTTACAGGAGAAAACCGAGAGTACATGGGTACCAACATTTCTC 1004

Qy        562 ArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSer 581
                 |||          :::   :::           |||   ||||||      |||
Db       1005 TTTCCA---------TCCACTTGGGAAAAGACAGTTGGAGGTACAGATTTAAAATCCCTG 1055

Qy        582 Gln---------TyrAsn---------GluAsp------MetLysLysPheArgLysMet 593
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                  :::          ||||||          ||||||      :::   ||||||      :::
Db       1056 GAACGATACCTCTACAATGTTGGAGGTGAAGACAAAATAGTACACAAGTTTGATTTTATA 1115

Qy        594 AlaLeu------GlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSer 611
                  :::          |||:::   ::::::          :::   |||:::   :::
Db       1116 ACGATTCTTGATGCAACTGAAAACTTCTCTGAAGCTAATAAGATTTCATCCTGCTCATAT 1175

Qy        612 AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGln 625
                 |||      :::|||      |||             ||||||
Db       1176 GAT---TCCGTGTAC---AAGGGACGGCTACAAAATGGACAA 1211
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```
RESULT 15
US-08-265-628-1
; Sequence 1, Application US/08265628
; Patent No. 5821094
;  GENERAL INFORMATION:
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Goring, Daphne
;    TITLE OF INVENTION:  S-LOCUS RECEPTOR KINASE GENE IN A
;    TITLE OF INVENTION:  SELF-INCOMPATIBLE BRASSICA NAPUS LINE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 W. Madison St.   Suite 3400
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,628
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/959,945
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/847,564
;      FILING DATE:  03-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien Ph.D., Donald J.
;      REGISTRATION NUMBER:  32,167
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-707-8889
;      TELEFAX:  312-707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2749 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  oleifera
;      INDIVIDUAL ISOLATE:  W1
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  S-locus
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2574
;    PUBLICATION INFORMATION:
;      AUTHORS:  GORING, DAPHNE
;      AUTHORS:  ROTHSTEIN, STEVEN J.
;      TITLE:  THE S-LOCUS RECEPTOR KINASE GENE IN A
;      TITLE:  SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A
;      TITLE:  FUNCTIONAL SERINE/THREONINE KINASE
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 2749
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US-08-265-628-1

Alignment Scores:

Pred. No.:	5.04e-16	Length:	2749
Score:	575.00	Matches:	154
Percent Similarity:	49.80%	Conservative:	94
Best Local Similarity:	30.92%	Mismatches:	160
Query Match:	16.65%	Indels:	91
DB:	1	Gaps:	14

US-10-086-464-2 (1-647) x US-08-265-628-1 (1-2749)

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Qy        130 SerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeu 149
              :::::::::|||   :::      ::::::||||||:::   :::
Db       1327 AACGCGAATGGGAAAACCATAGCGTTGATTGTTGGAGTTTGTGTT-------------- 1371

Qy        150 LeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGlu 169
              |||:::::::::   :::   |||   |||   |||:::|||:::::::|||   :::
Db       1372 CTGCTTCTTATGATCATGTTCTGC---CTCTGGAAAAGGAAACAAAAGCGAGCAAAAACA 1428

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
              |||   :::
Db       1429 ACTGCAACATCTATTGTAAAT---------------------------------------- 1449

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThr 209
                          ||||||:::|||               |||   ::::::
Db       1450 ------------------CGACAGAGAAAC-----------CAAGATTTGCTAATGAAC 1479

Qy        210 SerLeuProProProProLysAlaProSerProProArgGlnProProProProProPro 229
                 :::                    |||       ||||||   |||
Db       1480 GGGATG--------------ATACTATCAAGCAAGAGACAGTTGCCT------------ 1512

Qy        230 ProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProPro 249
                                      ::::::    :::   |||::::::
Db       1513 --------------ATAGAGAACAAAACTGAGGAATTGGAACTTCCATTGATA------ 1551

Qy        250 ProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla 269
                                                                |||   :::
Db       1552 ----------------------------------------GAGTTGGAAGCTGTTGTC 1569

Qy        270 ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrVal 289
              :::||||||      ||||||      |||   ||||||||||||||||||||   |||
Db       1570 AAAGCCACCGAAAATTTCTCCAATTGTAACAAACTCGGACAAGGTGGTTTCGGTATTGTT 1629

Qy        290 HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer 309
              :::||||||   |||      |||:::|||:::|||||||||:::|||          |||
Db       1630 TACAAGGGTAGATTACTTGATGGGCAAGAAATTGCGGTAAAAAGGCTATCAAAAACGTCG 1689

Qy        310 GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg 329
                ||||||     ||||||     ||||||   :::|||:::|||:::   |||
Db       1690 GTTCAAGGGACTGGTGAGTTTATGAATGAGGTGAGATTGATCGCGAGGCTTCAGCATATA 1749

Qy        330 HisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGlu 349
              :::||||||   :::::::|||   ||||||         :::::::::||||||||||||
Db       1750 AACCTTGTCCGAATTCTTGGCTGTTGCATTGAGGCAGACGAGAAGATGCTGGTATATGAG 1809

Qy        350 PheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArg---ProThrMet 368
              ::::::   |||   :::|||:::   :::|||   |||       |||      |||:::
Db       1810 TATTTAGAAAATTTAAGCCTCGATTCTTATCTCTTCGGAAATAAACGAAGCTCTACGTTA 1869

Qy        369 GluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis 388
                |||      |||      |||      |||   |||:::||||||   |||||||||
Db       1870 AATTGGAAGGACAGATTCAACATTACCAATGGTGTTGCTCGAGGACTTTTATATCTTCAT 1929

Qy        389 GluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAsp 408
              :::|||         :::|||||||||||||||:::|||   ||||||||||||:::|||
Db       1930 CAAGACTCACGGTTTAGGATAATCCACAGAGATATGAAAGTAAGTAACATTTTGCTTGAT 1989

Qy        409 PheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsn 428
                       |||::::::||||||||:::|||:::|||   :::
Db       1990 AAAAATATGACACCAAAGATCTCGGATTTTGGGATGGCCAGAATCTTTGCAAGGGACGAG 2049

Qy        429 ThrHisValSerThrArg---ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Db       2050 ACTGAAGCTAACACAAGGAAGGTGGTCGGAACTTACGGCTACATGTCTCCGGAGTACGCA 2109

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
                    |||      :::||||||||||||||||||||||||||||:::::::||||||
Db       2110 ATGGATGGGGTATTCTCGGAAAAATCAGATGTTTTCAGTTTTGGAGTCATTGTTCTTGAA 2169

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
              :::::::::|||:::|||                |||:::      :::::::::|||:::
Db       2170 ATTGTTAGTGGAAAAAGGAACAGAGGATTCTACAACTTGAACCACGAAAACAATCTTCTA 2229

Qy        488 Asp------TrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp--------- 502
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Db       2230 AGCTATGTATGGAGTCACTGGACGGAGGGAAGAGCGCTAGAAATTGTTGATCCAGTCATC 2289

Qy        503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
                 :::   |||:::                     :::      :::|||:::   :::
Db       2290 GTAGATTCATTGTCATCATTACCAGCAACC------TTTCAACCAAAAGAAGTTCTAAAA 2343

Qy        523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSer 542
                 :::                |||||:::      |||      ||||||   ||||||
Db       2344 TGCATACAAATTGGTCTCTTGTGTGTTCAAGAACGTGCAGAGCATAGACCAACGATGTCG 2403

Qy        543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562
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Db       2404 TCCGTGGTTTGGATGCTTGGAAGTGAAGCA------ACAGAGATTCCTGAGCCTACACCG 2457

Qy        563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySer--------------------- 575
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Db       2458 CCAGGTTATTCCCTCGGAAGAAGTCCTTATGAAAATAATCCTTCATCAAGTAGACATTGC 2517

Qy        576 ------------------------------------ThrAspTyrAspSerSerGln 582
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Db       2518 GACGACGACGAATCCTGGACGGTGAACCAGTACACCTGCTCAGACATCGATGCCCGGTAG 2577

Qy        583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Search completed: April 25, 2004, 01:02:38
Job time : 181 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 25, 2004, 00:01:06 ; Search time 638 Seconds
(without alignments)
4572.228 Million cell updates/sec

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Perfect score: 3453
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters: 5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3453	100.0	1944	14	US-10-086-464-1	Sequence 1, Appli
2	3453	100.0	2189	14	US-10-086-464-3	Sequence 3, Appli
3	2285.5	66.2	2451	13	US-10-424-599-95479	Sequence 95479, A
4	1870	54.2	1724	13	US-10-425-114-2326	Sequence 2326, Ap
5	1833	53.1	2880	13	US-10-425-114-33030	Sequence 33030, A
6	1833	53.1	2881	13	US-10-425-114-33031	Sequence 33031, A
7	1748.5	50.6	1902	14	US-10-086-464-10	Sequence 10, Appl
8	1748.5	50.6	1939	14	US-10-086-464-9	Sequence 9, Appli
9	1737.5	50.3	1424	13	US-10-425-114-9117	Sequence 9117, Ap
10	1687	48.9	2025	14	US-10-086-464-13	Sequence 13, Appl
11	1687	48.9	2104	14	US-10-086-464-12	Sequence 12, Appl
12	1539	44.6	2655	13	US-10-424-599-57846	Sequence 57846, A
13	1539	44.6	2655	13	US-10-425-114-7339	Sequence 7339, Ap
14	1437.5	41.6	2190	13	US-10-425-114-14127	Sequence 14127, A
15	1437	41.6	1500	13	US-10-425-114-6300	Sequence 6300, Ap
16	1437	41.6	1552	13	US-10-424-599-47702	Sequence 47702, A
17	1415.5	41.0	2196	14	US-10-086-464-7	Sequence 7, Appli
18	1415.5	41.0	2231	14	US-10-086-464-6	Sequence 6, Appli
19	1400.5	40.6	2261	14	US-10-086-464-15	Sequence 15, Appl
20	1399	40.5	2196	14	US-10-086-464-16	Sequence 16, Appl
21	1379	39.9	2508	13	US-10-425-114-25269	Sequence 25269, A
22	1335.5	38.7	1585	13	US-10-424-599-71008	Sequence 71008, A
23	1239	35.9	1588	13	US-10-425-114-35509	Sequence 35509, A
24	1238.5	35.9	1462	13	US-10-425-114-29328	Sequence 29328, A
25	1233.5	35.7	1134	13	US-10-425-114-36420	Sequence 36420, A
26	1210	35.0	1795	13	US-10-424-599-42232	Sequence 42232, A
27	1116.5	32.3	1179	13	US-10-425-114-4027	Sequence 4027, Ap
28	1116.5	32.3	1186	13	US-10-425-114-4273	Sequence 4273, Ap
29	1115.5	32.3	981	13	US-10-425-114-7549	Sequence 7549, Ap
30	921	26.7	729	13	US-10-425-114-12191	Sequence 12191, A
31	892.5	25.8	760	13	US-10-425-114-12314	Sequence 12314, A
32	866.5	25.1	951	13	US-10-425-114-1922	Sequence 1922, Ap
33	860.5	24.9	1777	13	US-10-425-114-24475	Sequence 24475, A
34	859.5	24.9	1817	13	US-10-425-114-30665	Sequence 30665, A
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44	804	23.3	2374	13	US-10-425-114-33063	Sequence 33063, A
45	802.5	23.2	2011	16	US-10-168-844-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-086-464-1
; Sequence 1, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1944
; TYPE: DNA

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;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1944)
US-10-086-464-1

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Score:                    3453.00         Matches:         647
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Best Local Similarity:    100.00%         Mismatches:      0
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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2
US-10-086-464-3
; Sequence 3, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2189
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2189)
;   OTHER INFORMATION:
US-10-086-464-3

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Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
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US-10-086-464-2 (1-647) x US-10-086-464-3 (1-2189)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 276

Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 336

Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656
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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
              |||||||||||||||||||||
Db       2017 GGTTATAGTGGACCTTCTCTT 2037

RESULT 3
US-10-424-599-95479
; Sequence 95479, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 95479
;   LENGTH: 2451
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_57229C.1
US-10-424-599-95479

Alignment Scores:
Pred. No.:              9e-140          Length:         2451
Score:                  2285.50         Matches:        450
Percent Similarity:     80.86%          Conservative:   74
Best Local Similarity:  69.44%          Mismatches:     97
Query Match:            66.19%          Indels:         27
DB:                     13              Gaps:           16

US-10-086-464-2 (1-647) x US-10-424-599-95479 (1-2451)

Qy         13 ProSerProProSerAsnSerThrThrThrThrProProProAla------SerAlaPro 30
              |||   ||||||      :::|||   ::::::||||||||||||      |||:::|||
Db        246 CCCCTCCCTCCGCCT---GCAACTCCGTCGTCACCTCCGCCGGCAACTCCGTCGTCTCCT 302

Qy         31 ProProThrThrProSerSerProProProProSerThrIleProThrSerProProPro 50
              ||||||   ||||||||||||||||||||      :::   |||:::|||||||||||||
Db        303 CCGCCGGCGACACCTTCTTCGCCACCTCCG------TCAACTCCTTCCTCGCCCCCTCCG 356

Qy         51 SerSerArgSerThrProSerAlaProProProSerProProThrProSerThrProGly 70
                  :::||||||||||||   |||||||||   |||:::   |||   |||
Db        357 ---------GCGACTCCCTCCGCTTCTCCACCGTCCACTCCTTCTGCTTCTCCTCCACCG 407

Qy         71 SerProProProLeuProGlnProSerProProAlaProThrThrProGlySerProPro 90
              |||   |||      |||      |||||||||:::   |||:::|||   |||||||||
Db        408 TCCACTCCAACCACGCCGTCAACTTCGCCGCCATCG---ACTTCTCCGCCGTCGCCGCCA 464

Qy         91 ------AlaProValThrProProThrArgAsnProProProSerValProGlyProPro 108
                    :::|||   :::|||||||:::                 |||   |||   ||||||
Db        465 TCGCACTCGCCGCCGTCGCCTCCCAGTGGCGGCGGAGGCGGCAGCACTCCGAGTCCACCG 524

Qy        109 SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSer 128
              |||      |||            |||         |||::::::|||||||||||||||
Db        525 TCCCGGAGCTCGCCCTCTCCTCCGTCCGGATCGAGACCGACCACTCCGTCGCCTCCGTCG 584

Qy        129 ProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAla 148
                  ||||||      :::|||||||||||||||||||||||||||:::|||   ||||||
Db        585 TCTTCCTCGTCGAGTATTTCGACCGGTGTGGTGGTGGGAATCGCCGTTGGGGCTGTGGCG 644

Qy        149 LeuLeuValIleValThrLeuIleCysLeuLeuCys---LysLysLysArgArgArgAsp 167
              :::|||::::::::::::::::::|||:::   |||   ||||||||||||||||||||
Db        645 GTTCTTCTTGTGTTGAGCATTCTCTGCATATGTTGCCGGAAGAAGAAGAGAAGACGTGAT 704

Qy        168 GluGluAspAlaTyrTyrValProProProProProPro---GlyProLysAlaGlyGly 186
              ||||||      ||||||   |||||||||   ||||||   |||||||||
Db        705 GAAGAG------TACTATGCTCCGCCGCCGCAACCGCCGCGGGGACCTAAA---GATGAT 755

Qy        187 ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHis 206
                  |||||||      :::||||||   |||   |||      ||||||   ||||||
Db        756 GCATATGGTGGTCCCCCACGTCAATGG---CAACACAATGTTCCCCCTCCTCAAGATCAT 812

Qy        207 ValValThrSerLeuProPro---------ProProLysAlaProSerProProArgGln 223
              ||||||:::   :::||||||         ||||||   ||||||
Db        813 GTGGTCTCAATGATGCCTCCAAAGCCATCGCCACCACCTGCTCCACCGGCTTATGCTGGT 872

Qy        224 ProProProProProProProProPheMetSerSerSerGly------GlySerAspTyr 241
                  ||||||||||||||||||||||:::|||||||||||||      |||||||:::|||
Db        873 CAACCTCCCCCACCACCGCCTCCTTTCATCAGCAGCAGTGGCGGATCTGGATCAAACTAT 932

Qy        242 SerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSer 261
              |||            ||||||||||||||||||||:::   ||||||||||||||||||
Db        933 TCAGGCGGTGAATTTCTTCCTCCTCCTTCTCCAGGAATTTCATTGGGATTCTCTAAGAGC 992

Qy        262 ThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeu 281
              ||||||||||||||||||||||||||||||||||:::|||||||||:::||||||||||||
Db        993 ACATTCACGTATGAGGAGTTGGCACGCGCAACTGATGGCTTCTCTGATGCCAACCTCCTT 1052

Qy        282 GlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAla 301
              |||||||||||||||||||||||||||||:::|||:::||||||:::||||||||||||||
Db       1053 GGACAAGGAGGATTTGGATATGTGCACAGAGGAATTCTTCCCAACGGCAAGGAGGTGGCA 1112

Qy        302 ValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGlu 321
              ||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db       1113 GTGAAGCAATTGAAGGCTGGAAGCGGGCAAGGGGAGCGTGAATTCCAAGCTGAAGTTGAG 1172

Qy        322 IleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGly 341
              ||||||||||||||||||||:::|||||||||||||||||||||||||||||||   |||
Db       1173 ATAATTAGCCGTGTCCATCACAAGCATCTTGTTTCTTTGGTTGGATACTGCATCACTGGG 1232

Qy        342 AlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361
              ::::::|||||||||||||||||||||||||||||||||||   ||||||   |||||||||
Db       1233 TCCCAGAGGCTGCTTGTTTATGAATTTGTTCCCAACAACACATTGGAATTCCATTTGCAT 1292

Qy        362 GlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
              |||:::|||||||||||||||:::|||   |||||||||:::|||||||||||||||||||
Db       1293 GGAAAAGGGCGACCTACCATGGATTGGCCCACAAGACTAAGAATTGCTTTAGGATCTGCT 1352

Qy        382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
              |||||||||:::|||||||||||||||||||:::|||||||||||||||||||||||||||
Db       1353 AAGGGACTGGCGTATCTTCATGAAGATTGTCATCCTAAGATCATCCATCGTGATATCAAA 1412

Qy        402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
              |||:::|||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCTGCCAACATCCTTCTGGATTTTAAGTTTGAAGCAAAGGTTGCAGATTTTGGTCTTGCA 1472

Qy        422 LysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyr 441
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Db       1473 AAGTTTTCTTCTGATGTCAATACCCATGTTTCTACTCGAGTGATGGGGACTTTTGGGTAT 1532

Qy        442 LeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPhe 461

Db       1533 TTGGCTCCAGAATATGCTTCTAGTGGAAAACTGACAGACAAATCAGATGTTTTCTCCTAT 1592

Qy        462 GlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyr 481

Db       1593 GGAGTCATGCTCCTCGAGTTAATAACCGGACGACGGCCAGTCGATAAAAATCAAACTTTC 1652

Qy        482 ValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501

Db       1653 ATGGAGGATAGTTTGGTAGACTGGGCTAGGCCTTTGCTCACACGAGCTTTGGAAGAGGAT 1712

Qy        502 AspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAla 521

Db       1713 GATTTTGATTCTATTATTGACCCAAGGCTCCAGAATGACTATGATCCTAATGAGATGGCA 1772

Qy        522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMet 541

Db       1773 CGAATGGTGGCTTCTGCTGCGGCTTGCATTCGTCATTCGGCAAAGCGTCGACCAAGGATG 1832

Qy        542 SerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMet 561

Db       1833 AGCCAGGTTGTTCGCGCTCTGGAAGGAGATGTCTCTCTAGCAGATCTTAACGAAGGAATT 1892

Qy        562 ArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSer 581

Db       1893 AGACCTGGACACAGCACTATGTACAGTTCTCAT---GAAAGCTCAGATTATGACACTGCA 1949

Qy        582 GlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsn 601

Db       1950 CAGTACAAGGAAGACATGAAAAAGTTCAGAAAAATGGCATTGGGAACTCAGGAGTATGGT 2009

Qy        602 AlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSer 621

Db       2010 GCAAGCAGTGAGTACAGTGCCGCTACAAGTGAGTATGGTTTAAACCCATCAGGCTCAAGT 2069

Qy        622 SerGluGly---------GlnThrThrArgGluMetGluMetGlyLysIleLysArgThr 638

Db       2070 AGTGAAGCACAGAGCCGCCAAACCACAAGGGAAATGGAAATGAGAAAGATGAAG---AAC 2126

Qy        639 GlyGlnGlyTyrSerGlyProSer 646

Db       2127 AATCAAGGTTTCAGTGGAAGTTCT 2150

RESULT 4
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
;   LENGTH: 1724
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

Alignment Scores:

Pred. No.:              6.61e-113       Length:         1724
Score:                  1870.00         Matches:        363
Percent Similarity:     79.85%          Conservative:   53
Best Local Similarity:  69.67%          Mismatches:     87
Query Match:            54.16%          Indels:         18
DB:                     13              Gaps:           9

US-10-086-464-2 (1-647) x US-10-425-114-2326 (1-1724)

Qy        139 ValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeu 158

Db          1 GTCGTGGGCGTGGCCGTCGGCGGCCTCGTGCTGCTGCTGCTCGCCAGCTTCATCTGCCTC 60

Qy        159 LeuCys------LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProPro 176

Db         61 TGCTGTCTCCGCAAGAAGCGCCGCCGCGCGCCGCCGCCGCCTCAGCACTACGGATACCCG 120

Qy        177 ProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArg 196

Db        121 CCGCCCCCGCCG---CCGTACAAGGAGGATCCATACGGTGGAACGTACCAGAGTTGG--- 174

Qy        197 GlnGlnAsnAla------ThrProProSerAspHisValValThrSerLeuPro---Pro 213

Db        175 CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAACATGTGGTCAAGATGCACCCTTCGCCT 234

Qy        214 ProProLysAlaProSerProProArgGlnProProProProProProProProPheMet 233

Db        235 CCGCCAGCATATGCCAATCGTCCTCCACAGCCGCCAGCGCCGCCACCACCAGCGATGCTA 294

Qy        234 SerSerSerGly------GlySerAspTyrSerAspArgProValLeuProProProSer 251

Db        295 AATAGTAGTGGTGGATCTGGTTCTAATTACTCTGGTGGCGAGATCCTACCTCCACCATCC 354

Qy        252 ProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAla 271

Db        355 CCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACATTCACCTACGAAGAGTTGTTGAGGGCT 414

Qy        272 ThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLys 291

Db        415 ACTGATGGATTCTCGGATGCTAATCTCCTTGGACAAGGTGGTTTTGGCTATGTTCACAGA 474

Qy        292 GlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGln 311

Db        475 GGATTGCTGCCTAATGGCAAAGAGATTGCTGTAAAACAACTGAAACTGGGAAGTGGCCAG 534

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331

Db        535 GGCGAGCGTGAGTTCCAGGCTGAGGTTGAGATTATCAGCCGAGTACATCACAAACACCTT 594

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351

Db        595 GTGTCTTTGGTTGGCTATTGCATTTCTGGAGGCAAGAGGCTGCTTGTCTATGAGTTTGTC 654

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371

Db        655 CCCAATAACACATTGGAATTCCACTTACATGCGAAAGATCGACCAACAATGGAGTGGCCT 714

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391

Db        715 GCTAGATTAAAGATCAGTTTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGC 774

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411

Db        775 CATCCAAAGATCATCCATCGTGACATAAAGGCATCTAACATTCTTCTTGACTTCCAATTT 834

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisVal 431

Db        835 GAAGCTAAGGTTGCTGATTTTGGACTTGCAAAGTTCACTACTGATAACAACACCCATGTT 894

Qy        432 SerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLys 451

Db        895 TCGACAAGAGTAATGGGCACCTTTGGGTATTTGGCACCTGAGTATGCATCTTCTGGCAAG 954
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Qy        452 LeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGly 471
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        955 CTAACAGAAAAATCTGATGTATTTTCCTTCGGAGTCATGCTTCTTGAGCTTATTACTGGG 1014

Qy        472 ArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArg 491
              ||||||||||||||||           |||:::|||||||||||||||||||||||||||
Db       1015 CGGCGACCAGTTGACACAACCCAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGG 1074

Qy        492 ProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMet 511
              |||||||||   ||||||   |||   |||:::::::::   |||   |||    ::::::
Db       1075 CCATTACTGATGCGAGCACTTGAGGATGGTGAATATGATGCTTTAGTGGATCCTCGGCTG 1134

Qy        512 AsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVal 531
                    ::::::      ||||||||||||||||:::|||||||||||||||||||||
Db       1135 GGAAAGGACTTCAATCCTAATGAGATGGCAAGAATGATAGCCTGTGCAGCTGCATGTGTA 1194

Qy        532 ArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsn 551
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db       1195 CGCCATTCTGCACGTCGTCGGCCACGTATGAGTCAGGTTGTTCGGGCTTTGGAGGGCAAT 1254

Qy        552 ValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSer 571
              |||||||||   ||||||||||||||:::|||||||||   |||       :::   |||
Db       1255 GTGTCTTTGGAGGACCTTAATGAAGGTGTTCGGCCTGGCCATAGCCGCTTCTTTGGGTCA 1314

Qy        572 TyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArg 591
              |||       |||:::||||||||||||   ||||||||||||||||||||||||||:::
Db       1315 TAC---AGCAGCTCCGATTACGATTCTGGCCAGTACAACGAGGACATGAAGAAGTTCAAG 1371

Qy        592 LysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSer 611
              |||||||||                              :::   :::||||||   |||||||||
Db       1372 AAGATGGCATTCAACAACAAC------TATACCAGCAGCCAATACAGCGCGCCAACCAGT 1425

Qy        612 AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGlu 631
              :::||||||      ||||||   ||||||||||||||      |||:::|||||||||
Db       1426 GAATATGGACAGATACCGTCTGCATCAAGCAGCGAGGGCCACCAGACGCAGGAGATGGAG 1485

Qy        632 MetGlyLysIleLysArgThrGly-----------------GlnGlyTyrSerGlyPro 645
                  |||   :::|||:::   |||                ||||||||||||
Db       1486 TCGGGTGCAATGAAGAAAGGTGGCTACAGTGGTGGCTACAGCTCAGGATACAGCGGAGCC 1545

Qy        646 Ser 646
              |||
Db       1546 TCG 1548
```

RESULT 5
US-10-425-114-33030
; Sequence 33030, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33030
; LENGTH: 2880
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B11_FLI
US-10-425-114-33030

Alignment Scores:

Pred. No.:	2.75e-110	Length:	2880
Score:	1833.00	Matches:	356
Percent Similarity:	79.80%	Conservative:	51
Best Local Similarity:	69.80%	Mismatches:	85
Query Match:	53.08%	Indels:	18
DB:	13	Gaps:	9

US-10-086-464-2 (1-647) x US-10-425-114-33030 (1-2880)

```
Qy        150 LeuValIleValThrLeuIleCysLeuLeuCys------LysLysLysArgArgArgAsp 167
              :::::::::   :::   |||||||||   |||      ||||||:::||||||
Db       1138 GTGCTGCTCGCCAGCTTCATCTGCCTCTGCTGTCTCCGCAAGAAGCGCCGCCGCGCGCCG 1197

Qy        168 GluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyPro 187
                        :::|||      ||||||||||||||   |||            |||
Db       1198 CCGCCGCCTCAGCACTACGGATACCCGCCGCCCCCGCCG---CCGTACAAGGAGGATCCA 1254

Qy        188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla------ThrProProSerAsp 205
              |||||||||      |||   |||   ||||||||||||         ||||||   :::
Db       1255 TATGGTGGAACGTACCAGAGTTGG---CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAA 1311

Qy        206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGlnPro 224
              |||||||||          |||   |||||||||          :::   |||   ||||||
Db       1312 CATGTGGTCAAGATGCACCCTTCGCCTCCGCCAGCATATGCCAATCGTCCTCCACAGCCG 1371

Qy        225 ProProProProProProProPheMetSerSerSerGly------GlySerAspTyrSer 242
              |||   ||||||||||||      ::::::|||||||||      ||||||:::||||||
Db       1372 CCAGCGCCGCCACCACCAGCGATGCTAAATAGTAGTGGTGGATCTGGTTCTAATTACTCT 1431

Qy        243 AspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThr 262
                  ::|||||||||||||||||||||||   ||||||||||||||||||||||||||
Db       1432 GGTGGCGAGATCCTACCTCCACCATCCCCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACA 1491

Qy        263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGly 282
              ||||||||||||||||||      |||||||||:::|||||||||:::||||||||||||
Db       1492 TTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCTAATCTCCTTGGA 1551

Qy        283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
              ||||||||||||||||||||||||||:::|||:::||||||:::||||||||:::||||||
Db       1552 CAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAAGAGATTGCTGTA 1611

Qy        303 LysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIle 322
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1612 AAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCTGAGGTTGAGATT 1671

Qy        323 IleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
              ||||||||||||||||:::|||||||||||||||||||||||||||||||:::|||
Db       1672 ATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGCATTTCTGGAGGC 1731

Qy        343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGly 362
              ||||||||||||||||||||||||||||||||||   ||||||   ||||||||
Db       1732 AAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTCCACTTACATGCG 1791

Qy        363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
              :::||||||||||||||||||      ||||||||||:::||||||:::||||||
Db       1792 AAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTGGGTGCTGCCAAG 1851

Qy        383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
              ||||||:::||||||||||||||||:::||||||||||||||||||||||||||||||
Db       1852 GGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCA 1911

Qy        403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
              ||||||||||:::|||||:::||||||||||||||||||||||||||||||||||||||
Db       1912 TCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGACTTTGGACTTGCAAAG 1971

Qy        423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
                    :::|||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1972 TTCACTACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTG 2031

Qy        443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db       2032 GCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGA 2091

Qy        463 ValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrVal 482
              |||:::|||||||||||||||||||||||||||||||||||||||||      |||:::
Db       2092 GTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATG 2151
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```
Qy       483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db      2152 GATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAA 2211

Qy       503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
Db      2212 TATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGA 2271

Qy       523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSer 542
Db      2272 ATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGT 2331

Qy       543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562
Db      2332 CAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGG 2391

Qy       563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582
Db      2392 CCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAG 2448

Qy       583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602
Db      2449 TACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACC 2502

Qy       603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622
Db      2503 AGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGC 2562

Qy       623 GluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly--------- 639
Db      2563 GAGGGCCACCAGACGCAGGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGT 2622

Qy       640 ---------GlnGlyTyrSerGlyProSer 646
Db      2623 GGCTACAGCTCAGGATACAGCGGAGCCTCG 2652

RESULT 6
US-10-425-114-33031
; Sequence 33031, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33031
;   LENGTH: 2881
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B12_FLI
US-10-425-114-33031

Alignment Scores:
Pred. No.:              2.75e-110      Length:         2881
Score:                  1833.00        Matches:        356
Percent Similarity:     79.80%         Conservative:   51
Best Local Similarity:  69.80%         Mismatches:     85
Query Match:            53.08%         Indels:         18
DB:                     13             Gaps:           9

US-10-086-464-2 (1-647) x US-10-425-114-33031 (1-2881)

Qy       150 LeuValIleValThrLeuIleCysLeuLeuCys------LysLysLysArgArgArgAsp 167

Db      1139 GTGCTGCTCGCCAGCTTCATCTGCCTCTGCTGTCTCCGCAAGAAGCGCCGCCGCGCGCCG 1198

Qy       168 GluGluAspAlaTyrTyrValProProProProProGlyProLysAlaGlyGlyPro 187
Db      1199 CCGCCGCCTCAGCACTACGGATACCCGCCGCCCCCGCCG---CCGTACAAGGAGGATCCA 1255

Qy       188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla------ThrProProSerAsp 205
Db      1256 TATGGTGGAACGTACCAGAGTTGG---CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAA 1312

Qy       206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGlnPro 224
Db      1313 CATGTGGTCAAGATGCACCCTTCGCCTCCGCCAGCATATGCCAATCGTCCTCCACAGCCG 1372

Qy       225 ProProProProProProProMetSerSerSerGly------GlySerAspTyrSer 242
Db      1373 CCAGCGCCGCCACCACCAGCGATGCTAAATAGTAGTGGTGGATCTGGTTCTAATTACTCT 1432

Qy       243 AspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThr 262
Db      1433 GGTGGCGAGATCCTACCTCCACCATCCCCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACA 1492

Qy       263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGly 282
Db      1493 TTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCTAATCTCCTTGGA 1552

Qy       283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
Db      1553 CAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAAGAGATTGCTGTA 1612

Qy       303 LysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIle 322
Db      1613 AAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCTGAGGTTGAGATT 1672

Qy       323 IleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
Db      1673 ATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGCATTTCTGGAGGC 1732

Qy       343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGly 362
Db      1733 AAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTCCACTTACATGCG 1792

Qy       363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
Db      1793 AAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTGGGTGCTGCCAAG 1852

Qy       383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
Db      1853 GGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCA 1912

Qy       403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
Db      1913 TCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGACTTTGGACTTGCAAAG 1972

Qy       423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
Db      1973 TTCACTACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTG 2032

Qy       443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
Db      2033 GCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGA 2092

Qy       463 ValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrVal 482
Db      2093 GTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATG 2152

Qy       483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db      2153 GATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAA 2212

Qy       503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
```

```
Db       2213 TATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGA 2272

Qy        523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSer 542

Db       2273 ATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGT 2332

Qy        543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562

Db       2333 CAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGG 2392

Qy        563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582

Db       2393 CCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAG 2449

Qy        583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602

Db       2450 TACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACC 2503

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622

Db       2504 AGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGC 2563

Qy        623 GluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly--------- 639

Db       2564 GAGGGCCACCAGACGCAGGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGT 2623

Qy        640 ---------GlnGlyTyrSerGlyProSer 646

Db       2624 GGCTACAGCTCAGGATACAGCGGAGCCTCG 2653

RESULT 7
US-10-086-464-10
; Sequence 10, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1902)
US-10-086-464-10

Alignment Scores:
Pred. No.:              5.75e-105      Length:          1902
Score:                  1748.50        Matches:          367
Percent Similarity:     69.67%         Conservative:      81
Best Local Similarity:  57.08%         Mismatches:       141
Query Match:            50.64%         Indels:            55
DB:                     14             Gaps:              16

US-10-086-464-2 (1-647) x US-10-086-464-10 (1-1902)

Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22

Db         19 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 78

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42

Db         79 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 129

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62

Db        130 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 189

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82

Db        190 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 246

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102

Db        247 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 306

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120

Db        307 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 357

Qy        121 ProSer------------------SerProSerProProSerPro------SerSerAsp 132

Db        358 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 417

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        418 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 477

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165

Db        478 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 537

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGly 185

Db        538 -----------GACTCCTTCTAC-----------------CCTGAACCCATGAAAGGA 567

Qy        186 GlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp 205

Db        568 AACCAATAT---------CAATACTA-TGGAAACAACAACAACAACAATGCTTCACAGAA 617

Qy        206 HisValValThrSerLeuProProProProLysAlaProSerProPro------------ 221

Db        618 ------TTATCCGAATTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGG 671

Qy        222 ------ArgGln-ProProProProProProProProPheMetSerSerSerGly----- 237

Db        672 TTGGGGAGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGA 731

Qy        238 -GlySerAspTyrSer------AspArgProValLeuProProProSerProGlyLeuVa 255

Db        732 TTCTTCCATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGC 791

Qy        255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275

Db        792 CCTCGGATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTT 851

Qy        275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295

Db        852 TACGGATGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCC 911

Qy        295 oSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGl 315

Db        912 TAGCGGGAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGA 971

Qy        315 uPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVa 335

Db        972 GTTTCAAGCTGAGGTCGATATCATTAGCCGTGTGCATCATCGGTATCTTGTTTCTTTGGT 1031

Qy        335 lGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAs 355

Db       1032 TGGATATTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAAC 1091

Qy        355 nLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLy 375
```

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Db       1092 TTTGGAATATCATCTTCATGGGAAAAATCTTCCGGTAATGGAGTTCTCCACTAGGTTGCG 1151

Qy        375 sIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIl 395

Db       1152 TATCGCCTTAGGTGCTGCGAAAGGACTCGCTTACCTTCACGAAGACTGCCATCCTCGGAT 1211

Qy        395 eIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysVa 415

Db       1212 CATTCACCGCGACATCAAGTCTGCAAATATTCTCTTGGACTTCAACTTTGATGCTATGGT 1271

Qy        415 lAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVa 435

Db       1272 GGCTGATTTTGGATTAGCTAAGTTAACATCTGATAACAACACTCATGTATCTACTCGTGT 1331

Qy        435 lMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLy 455

Db       1332 GATGGGAACTTTCGGATATCTAGCTCCAGAATATGCTTCAAGCGGTAAATTAACCGAGAA 1391

Qy        455 sSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVa 475

Db       1392 ATCCGATGTTTTCTCTTACGGAGTTATGTTATTGGAACTTATAACTGGAAAACGACCGGT 1451

Qy        475 lAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAs 495

Db       1452 TGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGCTCGGCCTCTTATGGC 1508

Qy        495 nArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTy 515

Db       1509 TCGCGCGCTAGAAGATGGAAACTTTAATGAGCTCGCAGATGCGAGGCTTGAAGGCAACTA 1568

Qy        515 rAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAl 535

Db       1569 CAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCCGCTGCTAGCATTCGTCATTCGGG 1628

Qy        535 aArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSe 555

Db       1629 GCGTAAACGTCCAAAGATGAGCCAGATAGTAAGAGCGTTAGAAGGAGAAGTGTCCTTAGA 1688

Qy        555 rAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySe 575

Db       1689 TGCTTTAAACGAAGGTGTGAAGCCAGGACACAGTAACGTTTACGGGTCATTGGGAGCAAG 1748

Qy        575 rThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLe 595

Db       1749 CTCGGATTATAGTCAGACATCTTACAATGCAGACATGAAGAAATTCAGACAGATAGCTTT 1808

Qy        595 uGlyThrGlnGluTyr---------AsnAlaThrGlyGluTyrSerAsnProThrSerAs 612

Db       1809 GTCGAGCCAAGAATTCCCAGTCAGTGACTGTGAAGGAACATCTAGTAATGATTCTAGAGA 1868

Qy        612 pTyrGly 614

Db       1869 TATGGGA 1875
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RESULT 8
US-10-086-464-9
; Sequence 9, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1939
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-086-464-9

Alignment Scores:

Pred. No.:	5.86e-105	Length:	1939
Score:	1748.50	Matches:	367
Percent Similarity:	69.67%	Conservative:	81
Best Local Similarity:	57.08%	Mismatches:	141
Query Match:	50.64%	Indels:	55
DB:	14	Gaps:	16

US-10-086-464-2 (1-647) x US-10-086-464-9 (1-1939)

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Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22

Db         36 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 95

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42

Db         96 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 146

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62

Db        147 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 206

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82

Db        207 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 263

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102

Db        264 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 323

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120

Db        324 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 374

Qy        121 ProSer-----------------SerProSerProProSerPro------SerSerAsp 132

Db        375 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 434

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 494

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165

Db        495 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 554

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGly 185

Db        555 -----------GACTCCTTCTAC-----------------CCTGAACCCATGAAAGGA 584

Qy        186 GlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp 205

Db        585 AACCAATAT---------CAATACTA-TGGAAACAACAACAACAACAATGCTTCACAGAA 634

Qy        206 HisValValThrSerLeuProProProProLysAlaProSerProPro------------ 221

Db        635 ------TTATCCGAATTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGG 688

Qy        222 ------ArgGln-ProProProProProProProProPheMetSerSerSerGly----- 237

Db        689 TTGGGGAGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGA 748

Qy        238 -GlySerAspTyrSer------AspArgProValLeuProProProSerProGlyLeuVa 255

Db        749 TTCTTCCATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGC 808
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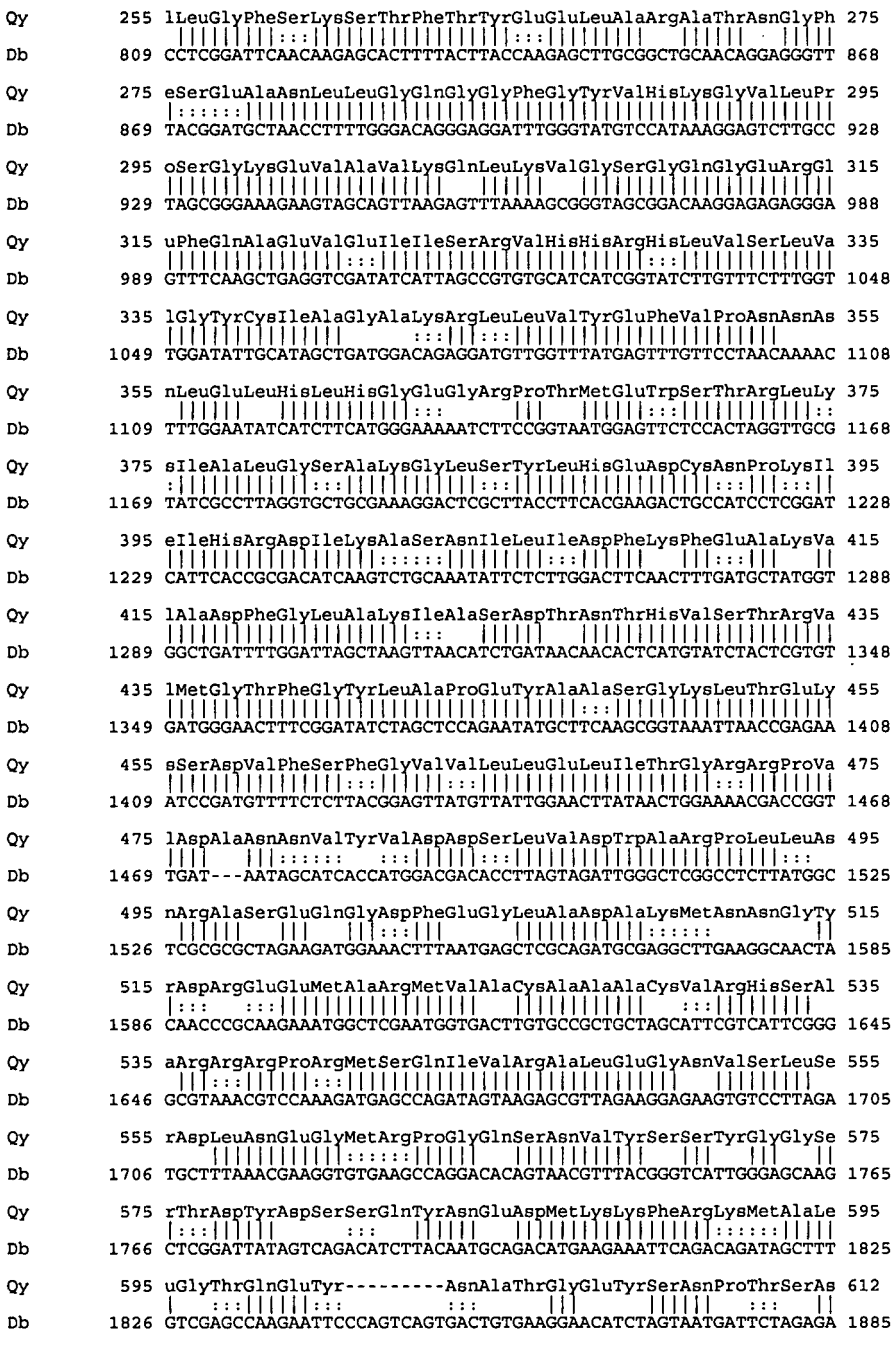

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Qy        255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275
Db        809 CCTCGGATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTT 868

Qy        275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295
Db        869 TACGGATGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCC 928

Qy        295 oSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGl 315
Db        929 TAGCGGGAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGA 988

Qy        315 uPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVa 335
Db        989 GTTTCAAGCTGAGGTCGATATCATTAGCCGTGTGCATCATCGGTATCTTGTTTCTTTGGT 1048

Qy        335 lGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAs 355
Db       1049 TGGATATTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAAC 1108

Qy        355 nLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLy 375
Db       1109 TTTGGAATATCATCTTCATGGGAAAAATCTTCCGGTAATGGAGTTCTCCACTAGGTTGCG 1168

Qy        375 sIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIl 395
Db       1169 TATCGCCTTAGGTGCTGCGAAAGGACTCGCTTACCTTCACGAAGACTGCCATCCTCGGAT 1228

Qy        395 eIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysVa 415
Db       1229 CATTCACCGCGACATCAAGTCTGCAAATATTCTCTTGGACTTCAACTTTGATGCTATGGT 1288

Qy        415 lAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVa 435
Db       1289 GGCTGATTTTGGATTAGCTAAGTTAACATCTGATAACAACACTCATGTATCTACTCGTGT 1348

Qy        435 lMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLy 455
Db       1349 GATGGGAACTTTCGGATATCTAGCTCCAGAATATGCTTCAAGCGGTAAATTAACCGAGAA 1408

Qy        455 sSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVa 475
Db       1409 ATCCGATGTTTTCTCTTACGGAGTTATGTTATTGGAACTTATAACTGGAAAACGACCGGT 1468

Qy        475 lAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAs 495
Db       1469 TGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGCTCGGCCTCTTATGGC 1525

Qy        495 nArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTy 515
Db       1526 TCGCGCGCTAGAAGATGGAAACTTTAATGAGCTCGCAGATGCGAGGCTTGAAGGCAACTA 1585

Qy        515 rAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAl 535
Db       1586 CAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCCGCTGCTAGCATTCGTCATTCGGG 1645

Qy        535 aArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSe 555
Db       1646 GCGTAAACGTCCAAAGATGAGCCAGATAGTAAGAGCGTTAGAAGGAGAAGTGTCCTTAGA 1705

Qy        555 rAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySe 575
Db       1706 TGCTTTAAACGAAGGTGTGAAGCCAGGACACAGTAACGTTTACGGGTCATTGGGAGCAAG 1765

Qy        575 rThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLe 595
Db       1766 CTCGGATTATAGTCAGACATCTTACAATGCAGACATGAAGAAATTCAGACAGATAGCTTT 1825

Qy        595 uGlyThrGlnGluTyr---------AsnAlaThrGlyGluTyrSerAsnProThrSerAs 612
Db       1826 GTCGAGCCAAGAATTCCCAGTCAGTGACTGTGAAGGAACATCTAGTAATGATTCTAGAGA 1885

Qy        612 pTyrGly 614
Db       1886 TATGGGA 1892
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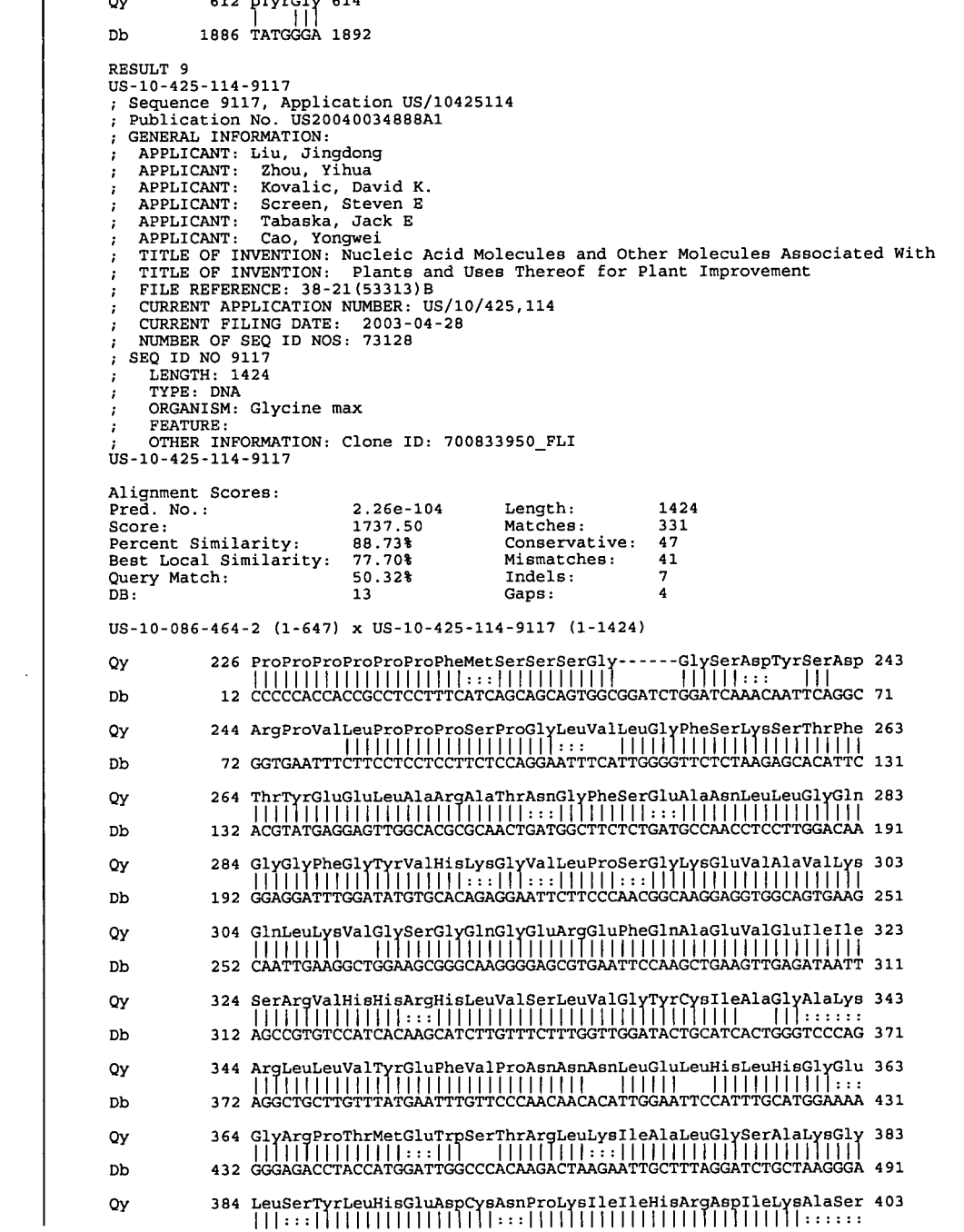
RESULT 9
US-10-425-114-9117
; Sequence 9117, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9117
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700833950_FLI
US-10-425-114-9117

Alignment Scores:

Pred. No.:	2.26e-104	Length:	1424
Score:	1737.50	Matches:	331
Percent Similarity:	88.73%	Conservative:	47
Best Local Similarity:	77.70%	Mismatches:	41
Query Match:	50.32%	Indels:	7
DB:	13	Gaps:	4

US-10-086-464-2 (1-647) x US-10-425-114-9117 (1-1424)



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Qy        226 ProProProProProProPheMetSerSerSerGly------GlySerAspTyrSerAsp 243
Db         12 CCCCCACCACCGCCTCCTTTCATCAGCAGCAGTGGCGGATCTGGATCAAACAATTCAGGC 71

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
Db         72 GGTGAATTTCTTCCTCCTCCTTCTCCAGGAATTTCATTGGGGTTCTCTAAGAGCACATTC 131

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
Db        132 ACGTATGAGGAGTTGGCACGCGCAACTGATGGCTTCTCTGATGCCAACCTCCTTGGACAA 191

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
Db        192 GGAGGATTTGGATATGTGCACAGAGGAATTCTTCCCAACGGCAAGGAGGTGGCAGTGAAG 251

Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
Db        252 CAATTGAAGGCTGGAAGCGGGCAAGGGGAGCGTGAATTCCAAGCTGAAGTTGAGATAATT 311

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
Db        312 AGCCGTGTCCATCACAAGCATCTTGTTTCTTTGGTTGGATACTGCATCACTGGGTCCCAG 371

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGlu 363
Db        372 AGGCTGCTTGTTTATGAATTTGTTCCCAACAACACATTGGAATTCCATTTGCATGGAAAA 431

Qy        364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db        432 GGGAGACCTACCATGGATTGGCCCACAAGACTAAGAATTGCTTTAGGATCTGCTAAGGGA 491

Qy        384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
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Db        492 CTGGCGTATCTTCATGAAGATTGTCATCCTAAGATCATCCATCGTGATATCAAATCTGCC 551

Qy        404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423

Db        552 AACATCCTTCTGGATTTTAAGTTTGAAGCAAAGGTTGCAGATTTTGGTCTTGCAAAGTTT 611

Qy        424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443

Db        612 TCTTCTGATGTCAATACCCATGTTTCTACTCGAGTGATGGGGACTTTTGGGTATTTGGCT 671

Qy        444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463

Db        672 CCAGAATATGCTTCTAGTGGAAAACTCACAGACAAATCAGATGTTTTCTCCTATGGAATC 731

Qy        464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAsp 483

Db        732 ATGCTCCTTGAGTTAATAACCGGACGACGGCCAGTTGATAAAAATCAAACTTACATGGAG 791

Qy        484 AspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPhe 503

Db        792 GATAGTTTGGTAGATTGGGCTAGGCCTTTGCTCACACGAGCTTTGGAAGAGGATGATTTT 851

Qy        504 GluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMet 523

Db        852 GATTCTATTATTGACCCAAGGCTCCAGAATGACTATGATCCTCATGAGATGGCACGAATG 911

Qy        524 ValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln 543

Db        912 GTGGCTTCTGCTGCGGCTTGCATACGTCATTCGGCAAAGCGTCGACCAAGGATGAGCCAG 971

Qy        544 IleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgPro 563

Db        972 GTTGTCCGCGCTCTCGAAGGAGATGTCTCTCTAGCAGATCTGAATGAAGGAATAAGACCT 1031

Qy        564 GlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyr 583

Db       1032 GGACACAGCACTATGTATAGTTCTCAT---GAAAGCTCAGATTATGACACTGCACAGTAC 1088

Qy        584 AsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThr 603

Db       1089 AAGGAAGACATGAAAAAGTTCAGGAAAATGGCATTGGGAACTCAGGAGTATGGTGCAAGC 1148

Qy        604 GlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGlu 623

Db       1149 AGTGAGTACAGTGCCGCTACAAGTGAGTATGGTTTAAACCCATCAGGCTCAAGTAGTGAA 1208

Qy        624 Gly---------GlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640

Db       1209 GCACAGAGCCGCCAAACCACAAGGGAAATGGAAATGAGAAAGATGAAG---AACAATCAA 1265

Qy        641 GlyTyrSerGlyProSer 646

Db       1266 GGTTTCAGTGGAAGTTCT 1283

RESULT 10
US-10-086-464-13
; Sequence 13, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 2025
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2025)
US-10-086-464-13

Alignment Scores:
Pred. No.:              6.08e-101      Length:          2025
Score:                  1687.00        Matches:         368
Percent Similarity:     63.99%         Conservative:    87
Best Local Similarity:  51.76%         Mismatches:      142
Query Match:            48.86%         Indels:          114
DB:                     14             Gaps:            25

US-10-086-464-2 (1-647) x US-10-086-464-13 (1-2025)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20

Db         16 GTGGATTCATCTCCTGCCCCTGAAACC---TCAAATGGGACACCACCGTCAAACGGAACA 72

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40

Db         73 TCG---------CCGTCTAATGAGTCATCGCCGCCAACACCACCTTCTTCACCACCACCA 123

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60

Db        124 TCATCA---------ATATCTGCTCCTCCGCCAGATATCTCCGCTTCTTTTTCACCGCCG 174

Qy         61 ProSerProProThr--------------ProSerThrProGlySerProProProLeu 75

Db        175 CCTGCACCACCAACGCAAGAAACGTCACCTCCTACATCTCCGTCCTCATCGCCGCCTGTT 234

Qy         76 --------------ProGln-----------ProSerProProAlaPro------Thr 84

Db        235 GTAGCTAATCCGTCACCGCAGACTCCAGAGAATCCTTCTCCACCTGCACCTGAAGGCTCA 294

Qy         85 ThrProGlySerProProAla---ProValThrPro-----------ProThrArgAsn 99

Db        295 ACTCCTGTAACGCCACCTGCACCACCACAAACACCGTCGAACCAATCACCGGAAAGACCA 354

Qy        100 ProProPro---------------------------------------------------- 102

Db        355 ACTCCTCCTTCTCCTGGTGCCAATGATGACCGAAACAGAACCAATGGCGGAAACAACAAC 414

Qy        103 ---------SerValProGlyProProSerAsnProSerArg---------GluGlyGly 116

Db        415 AGAGACGGCTCCACACCATCACCACCGTCGTCAGGGAACAGAACTTCCGGTGACGGTGGC 474

Qy        117 SerProArgProProSerSerProSerProProSerProSerSerAspGlyLeuSerThr 136

Db        475 TCACCTTCACCACCTCGGTCGATAAGCCCTCCTCAGAATAGTGGAGATTCAGACTCATCA 534

Qy        137 GlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIle 156

Db        535 TCG---------GGGCTT-----------------TTGCTTCTACTTGCAGTGTGTATT 567

Qy        157 CysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAla------------Tyr 172

Db        568 TGCATCTGTTGCAACAGGAAGAAGAAGAAGAAATCTCCTCAGGTCAACCACATGCACTAC 627

Qy        173 TyrValProProProProProProGlyProLysAla---GlyGlyProTyrGlyGlyGln 191

Db        628 TACAATAACAATCCTTATGGAGGAGCACCCTCAGGTAATGGTGGTTATTACAAGGGA--- 684

Qy        192 GlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeu 211

Db        685 ----------------------------ACACCTCAAGATCATGTGGTG---AATATG 711

Qy        212 ProProProProLysAlaProSerProProArgGlnProProProProProProPro 231
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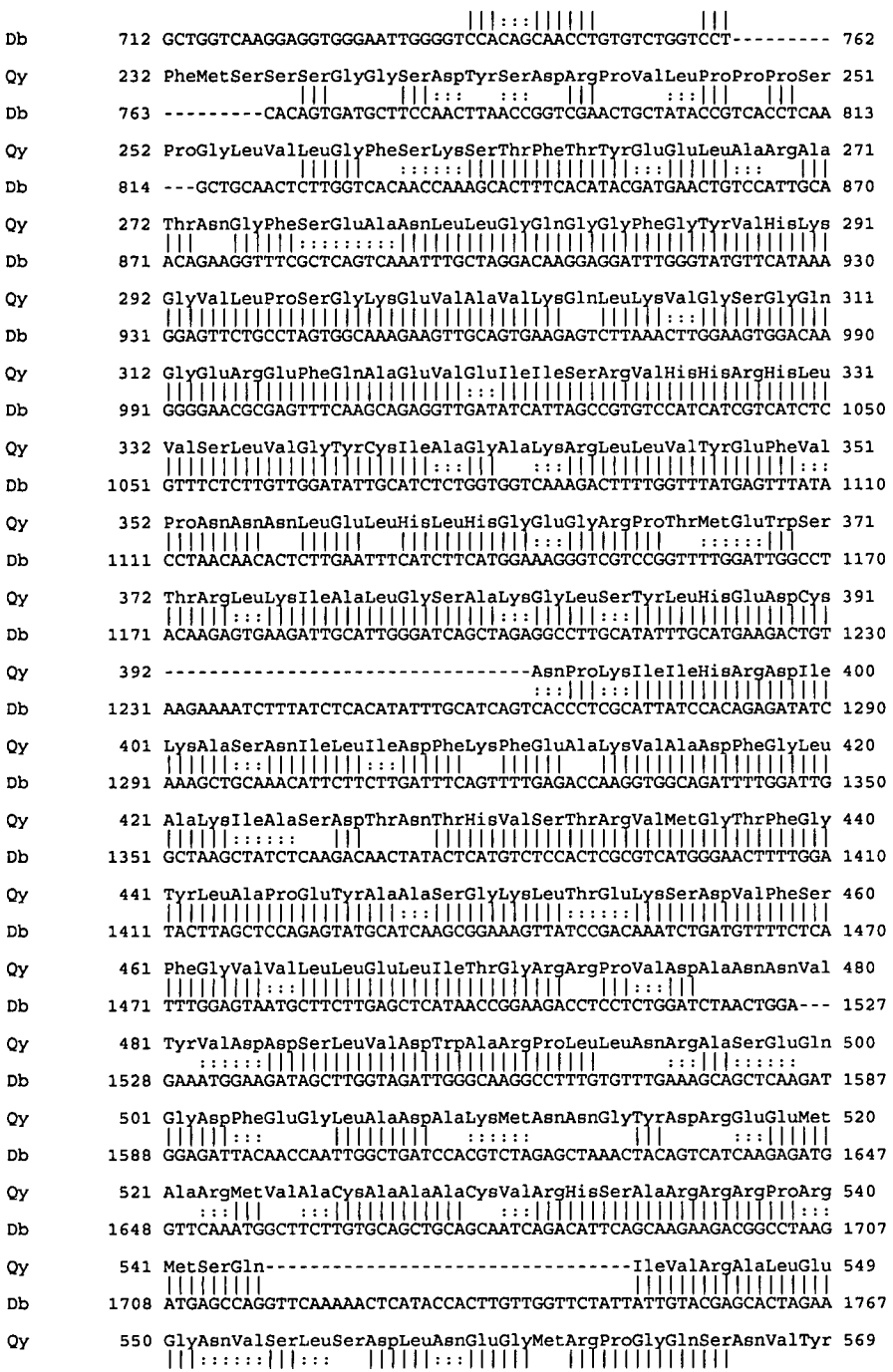
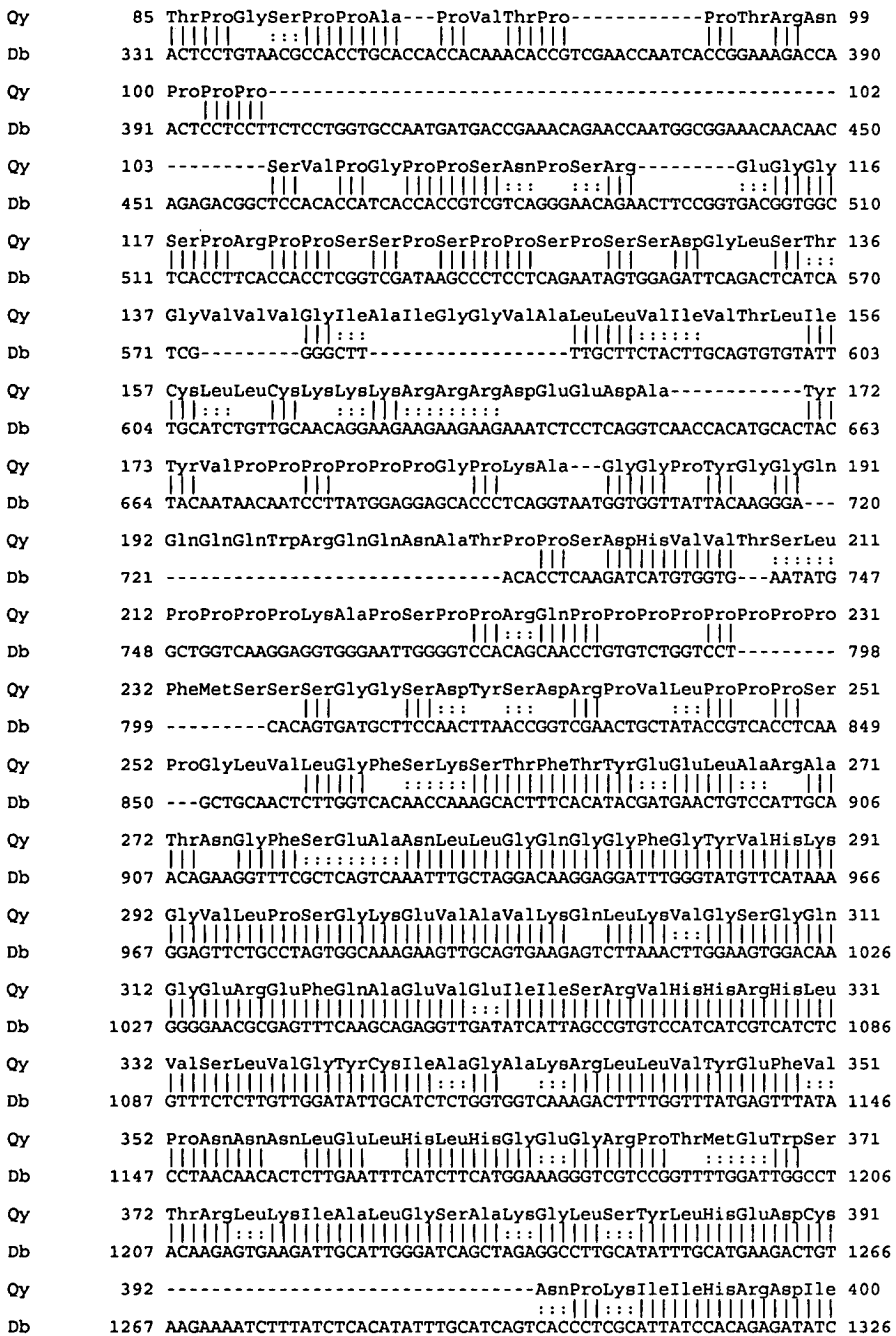


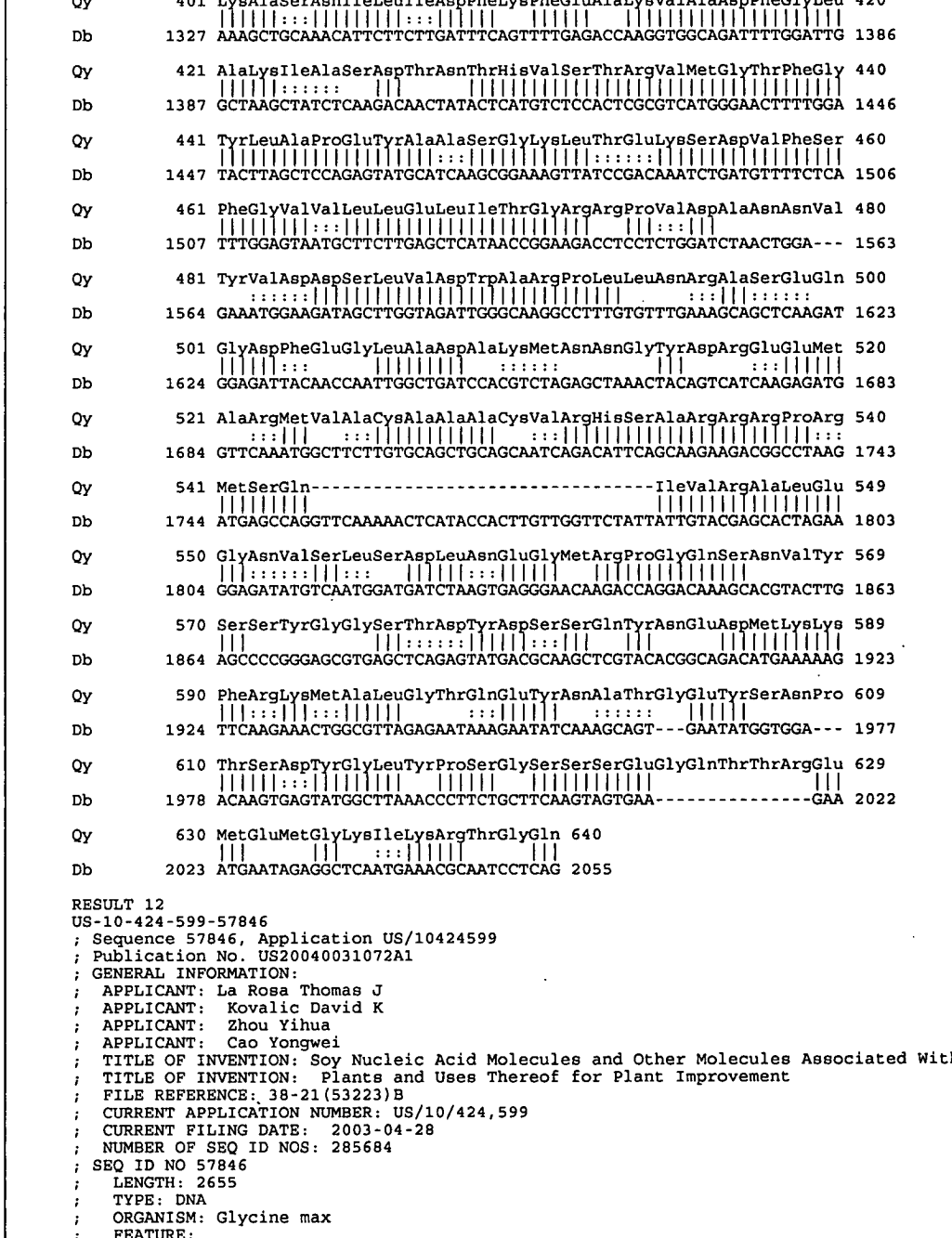
RESULT 11
US-10-086-464-12
; Sequence 12, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-086-464-12

Alignment Scores:

Pred. No.:	6.31e-101	Length:	2104
Score:	1687.00	Matches:	368
Percent Similarity:	63.99%	Conservative:	87
Best Local Similarity:	51.76%	Mismatches:	142
Query Match:	48.86%	Indels:	114
DB:	14	Gaps:	25

US-10-086-464-2 (1-647) x US-10-086-464-12 (1-2104)





RESULT 12
US-10-424-599-57846
; Sequence 57846, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57846
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23247C.1

US-10-424-599-57846

Alignment Scores:

Pred. No.:	3.3e-91	Length:	2655
Score:	1539.00	Matches:	341
Percent Similarity:	55.19%	Conservative:	95
Best Local Similarity:	43.16%	Mismatches:	141
Query Match:	44.57%	Indels:	213
DB:	13	Gaps:	19

US-10-086-464-2 (1-647) x US-10-424-599-57846 (1-2655)

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Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSer------ 19
              ||||||:::|||:::      |||   :::||||||||||||||||||:::|||
Db         98 TCATCTTCTCCAACA---AACACTTCCACCCCACCATCACCTCCCAGTTCTTCTCAGCCT 154

Qy         20 ------------ThrThrThrThrProProProAlaSerAlaPro---ProProThrThr 34
                         |||   |||       |||   :::   ||||||      |||:::
Db        155 AATCAAACACAAACACAAACACAAACACCCAATTCCCCTGCTCCTTCATCTCCTTCTGAC 214

Qy         35 ProSerSerProPro------ProProSerThrIleProThrSerProProProSerSer 52
              ||||||:::||||||      ||||||      :::|||   :::||||||||||||
Db        215 CCTTCTGCTCCACCTCCTTCTCCTCCTCAGGCAGTGCCATTAACCCCTCCTCCTTCCATA 274

Qy         53 ArgSerThrPro---------SerAlaProProProSerProProThrProSerThrPro 69
                 :::|||         |||   |||||||||:::   |||   ||||||   |||
Db        275 TCACTGTCTCCTCCACCATCATCTACACCACCACCAACTTTGCCCCCTCCATCACCACCT 334

Qy         70 GlySerProProProLeuPro--------------------------------GlnPro 78
                 ||||||||||||||||||                                |||
Db        335 GATTCTCCACCACCATTGCCACCTGCATCTCCAACCCCACCAGTTACAACATCTCCCCCC 394

Qy         79 SerProProAlaProThrThrProGlySerProProAlaProValThrProProThrArg 98
              |||||||||      |||:::|||   ||||||||||||      :::||||||
Db        395 TCACCACCAGTTACAACATCTCCCCCCTCACCACCAGCTACCACATCCCCTCCTCCAGCT 454

Qy         99 AsnProProProSerValPro------GlyProProSerAsnProSerArgGluGlyGly 116
                    |||||||||:::|||         |||||||||   |||:::                |||
Db        455 GAAACTCCACCTTCCCTTCCAAATTTGTCTCCACCATCTCCACCAGCC---------GGT 505

Qy        117 SerProArgPro-------------------------------------ProSerSerPro 124
              ||||||   |||                                     |||   ||||||
Db        506 TCCCCTCCTCCTCAATCACCTCCCACAACAATTCCACCTCCCTCTCGACCGATTTCGCCA 565

Qy        125 SerProProSerProSer---------------------------------------- 130
              |||||||||   |||:::
Db        566 TCTCCTCCTCCTCCGGCCAATTTTCCAAGGCCACCAACCACTAGAACTCCTCCAGAGAAA 625

Qy        130 ---------------------------------------------------------- 130

Db        626 GAAAATCCACCAAAAACTACTCCTTCACATGCATCTCCTCCATCAGTTTCTGAAACTCCT 685

Qy        130 ---------------------------------------------------------- 130

Db        686 CCTAAACCTCCTTCCTCTGATGTTCCCCCTCCATCCACATTGCCTTCAACTCCTCCTTCA 745

Qy        130 ---------------------------------------------------------- 130

Db        746 GACCCTTCAGGATCTTCACCTCCAGCTTCTTTGCCTGATCCCCCAACTAATAAAACAGTG 805

Qy        130 ---------------------------------------------------------- 130

Db        806 GTGGGGGGTCCGAAGGTGTCGCTACCCTCTCTTCCAACTGAGAAACCCACTGCTAGACCT 865

Qy        131 ------------------------------------------------SerAspGlyLeu 134
                                                             |||   ||||||
Db        866 ACTAATGATGGTACTAACAGTATGTCTTCAAACAACACACCTTCACATTCTGGAGGGTTG 925

Qy        135 SerThrGly------ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIle 152
              |||||||||      |||   :::|||||||   :::|||   :::   |||   ::::::
Db        926 AGCACTGGAGGATCTGTGGCTATTGGAATTGTAGTTGGTTTTATTGTCCTCAGCCTTCTT 985

Qy        153 ValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAlaTyr 172
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                 |||       :::           |||||||||::::::
Db         986 GTTATGGCTGTGTGGTTTGCACAGAAGAAAAAGAAGAAGGGAACAGGATCAAGAGGTAGT 1045

Qy         173 TyrValProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGln 192
                 |||      |||   |||
Db        1046 TATGCTGCTCCTTCTCCA---------------------------------------- 1063

Qy         193 GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212
                                                  |||   |||         :::|||
Db        1064 --------------------------TTTACCTCATCCCACAATTCAGGTACCTTATTC 1096

Qy         213 ProProProLysAlaProSerProProArgGlnProProProProProProProProPhe 232
                    |||::::::|||:::                                     |||
Db        1097 TTGAGGCCGCAGTCTCCGGCC--------------------------------AACTTT 1123

Qy         233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro 252
                 :::   |||       |||||||||:::           |||       |||       |||
Db        1124 TTAGGTAGTGGCTCTGGTAGTGATTTT------------GTATATTCTCCATCAGAGCCT 1171

Qy         253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272
                 |||   |||         |||:::|||   ||||||||||||||||||   :::|||||||
Db        1172 GGTGGTGTA---AGTAGTTCAAGATCATGGTTCACATATGAAGAACTTATTCAAGCTACA 1228

Qy         273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
                 ||||||||||||      ||||||||||||:::||||||||||||   |||:::||||||
Db        1229 AATGGGTTTTCAGCACAAAATTTGTTGGGAGAAGGTGGATTTGGCTGTGTTTATAAAGGT 1288

Qy         293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312
                 :::|||      |||:::||||||||||||||||||||||:::|||   |||||||||
Db        1289 TTGCTGATAGATGGAAGAGAAGTAGCTGTGAAACAGCTCAAAATTGGTGGTGGGCAAGGG 1348

Qy         313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
                 ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        1349 GAACGCGAATTCAGGGCAGAAGTTGAGATTATTAGCCGTGTACATCATCGTCATCTGGTT 1408

Qy         333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
                 |||||||||||||||||||||:::      :::||||||||||||||:::::|||||||
Db        1409 TCTTTAGTTGGTTACTGTATATCCGAGCATCAGAGATTGCTTGTATATGACTATGTTCCC 1468

Qy         353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372
                 |||:::   |||      |||||||||||||||   ||||||   ::::::|||   |||
Db        1469 AACGATACTCTTCATTACCATCTCCACGGTGAAAATAGACCAGTTCTAGATTGGCCTACC 1528

Qy         373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
                 |||:::|||:::|||   |||:::|||:::|||::::::|||||||||||||||||:::
Db        1529 AGAGTCAAGGTTGCTGCTGGTGCAGCTCGTGGAATAGCTTACTTGCATGAAGACTGTCAT 1588

Qy         393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
                 |||:::|||||||||||||||||||:::|||||||||||:::|||      :::|||
Db        1589 CCACGCATTATTCATCGAGATATTAAGTCATCAAACATCCTACTTGATCTCAACTATGAA 1648

Qy         413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
                 |||:::|||:::|||||||||||||||||:::|||   |||:::|||||||||||:::
Db        1649 GCTCAAGTTTCGGACTTTGGGCTTGCAAAATTGGCATTAGATTCAAATACACATGTAACT 1708

Qy         433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
                 ||||||||||||||||||||||||||:::|||||||||||||||   ||||||||||||
Db        1709 ACACGTGTAATGGGAACCTTTGGGTACATGGCACCAGAATATGCGACAAGTGGAAAACTT 1768

Qy         453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472
                 |||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        1769 ACTGAAAAGTCTGATGTATATTCTTTTGGGGTTGTGCTTTTGGAGCTAATTACAGGTCGG 1828

Qy         473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
                 :::|||||||||||:::           |||:::||||||||:::|||||||||||||
Db        1829 AAGCCTGTAGATGCATCTCAACCAATTGGTGATGAGAGCCTGGTTGAATGGGCTCGACCT 1888

Qy         493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
                 ||||||      |||   :::      |||||||||   |||   |||   ::::::
Db        1889 CTGTTGACGGAAGCACTTGACAATGAGGACTTTGAAATTTTGGTGGATCCAAGACTGGGG 1948

Qy         513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
                 |||||||||   ||||||   ||||||:::      ||||||||||||||||||
```

```
Db       1949 AAGAACTACGATAGAAATGAAATGTTTCGGATGATCGAGGCTGCCGCAGCCTGTGTACGC 2008

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552

Db       2009 CACTCATCGGTGAAGAGACCACGCATGAGTCAGGTGGTGAGAGCTTTAGATTCCTTGGAT 2068

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572

Db       2069 GAGTTTACGGATCTCAATAACGGAATGAAACCGGGACAGAGTTCGGTG------------ 2116

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592

Db       2117 --------------TTTGATTCGGCGCAGCAATCTGCACAAATCAGAATGTTTAGGAGG 2161

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612

Db       2162 ATGGCTTTTGGGAGCCAAGAT------AGTTCCGGTTTCTTCAATGAGTCTCAGAGTAGC 2215

Qy        613 Tyr-GlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMe 632

Db       2216 TGGAGGAGTA-----------------------GAGATCACGACCCAACAACTGTCTTC 2251

Qy        632 tGlyLysIleLysArgThrGlyGlnGly 641

Db       2252 TCCCAAAATAAAA---CTGGGCATGGGA 2276

RESULT 13
US-10-425-114-7339
; Sequence 7339, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7339
;   LENGTH: 2655
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700652889_FLI
US-10-425-114-7339

Alignment Scores:
Pred. No.:              3.3e-91       Length:        2655
Score:                  1539.00       Matches:       341
Percent Similarity:     55.19%        Conservative:  95
Best Local Similarity:  43.16%        Mismatches:    141
Query Match:            44.57%        Indels:        213
DB:                     13            Gaps:          19

US-10-086-464-2 (1-647) x US-10-425-114-7339 (1-2655)

Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSer------ 19

Db         98 TCATCTTCTCCAACA---AACACTTCCACCCCACCATCACCTCCCAGTTCTTCTCAGCCT 154

Qy         20 ------------ThrThrThrThrProProProAlaSerAlaPro---ProProThrThr 34

Db        155 AATCAAACACAAACACAAACACAAACACCCAATTCCCCTGCTCCTTCATCTCCTTCTGAC 214

Qy         35 ProSerSerProPro------ProProSerThrIleProThrSerProProProSerSer 52

Db        215 CCTTCTGCTCCACCTCCTTCTCCTCCTCAGGCAGTGCCATTAACCCCTCCTCCTTCCATA 274

Qy         53 ArgSerThrPro---------SerAlaProProProSerProProThrProSerThrPro 69

Db        275 TCACTGTCTCCTCCACCATCATCTACACCACCACCAACTTTGCCCCCTCCATCACCACCT 334

Qy         70 GlySerProProProLeuPro--------------------------------GlnPro 78

Db        335 GATTCTCCACCACCATTGCCACCTGCATCTCCAACCCCACCAGTTACAACATCTCCCCCC 394

Qy         79 SerProProAlaProThrThrProGlySerProProAlaProValThrProProThrArg 98

Db        395 TCACCACCAGTTACAACATCTCCCCCCTCACCACCAGCTACCACATCCCCTCCTCCAGCT 454

Qy         99 AsnProProProSerValPro------GlyProProSerAsnProSerArgGluGlyGly 116

Db        455 GAAACTCCACCTTCCCTTCCAAATTTGTCTCCACCATCTCCACCAGCC---------GGT 505

Qy        117 SerProArgPro------------------------------------ProSerSerPro 124

Db        506 TCCCCTCCTCCTCAATCACCTCCCACAACAATTCCACCTCCCTCTCGACCGATTTCGCCA 565

Qy        125 SerProProSerProSer---------------------------------------- 130

Db        566 TCTCCTCCTCCTCCGGCCAATTTTCCAAGGCCACCAACCACTAGAACTCCTCCAGAGAAA 625

Qy        130 ---------------------------------------------------------- 130

Db        626 GAAAATCCACCAAAAACTACTCCTTCACATGCATCTCCTCCATCAGTTTCTGAAACTCCT 685

Qy        130 ---------------------------------------------------------- 130

Db        686 CCTAAACCTCCTTCCTCTGATGTTCCCCCTCCATCCACATTGCCTTCAACTCCTCCTTCA 745

Qy        130 ---------------------------------------------------------- 130

Db        746 GACCCTTCAGGATCTTCACCTCCAGCTTCTTTGCCTGATCCCCCAACTAATAAAACAGTG 805

Qy        130 ---------------------------------------------------------- 130

Db        806 GTGGGGGGTCCGAAGGTGTCGCTACCCTCTCTTCCAACTGAGAAACCCACTGCTAGACCT 865

Qy        131 ------------------------------------------------SerAspGlyLeu 134

Db        866 ACTAATGATGGTACTAACAGTATGTCTTCAAACAACACACCTTCACATTCTGGAGGGTTG 925

Qy        135 SerThrGly------ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIle 152

Db        926 AGCACTGGAGGATCTGTGGCTATTGGAATTGTAGTTGGTTTTATTGTCCTCAGCCTTCTT 985

Qy        153 ValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAlaTyr 172

Db        986 GTTATGGCTGTGTGGTTTGCACAGAAGAAAAAGAAGAAGGGAACAGGATCAAGAGGTAGT 1045

Qy        173 TyrValProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGln 192

Db       1046 TATGCTGCTCCTTCTCCA---------------------------------------- 1063

Qy        193 GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212

Db       1064 --------------------------TTTACCTCATCCCACAATTCAGGTACCTTATTC 1096

Qy        213 ProProProLysAlaProSerProProArgGlnProProProProProProProPhe 232

Db       1097 TTGAGGCCGCAGTCTCCGGCC--------------------------------AACTTT 1123

Qy        233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro 252

Db       1124 TTAGGTAGTGGCTCTGGTAGTGATTTT-----------GTATATTCTCCATCAGAGCCT 1171

Qy        253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272

Db       1172 GGTGGTGTA---AGTAGTTCAAGATCATGGTTCACATATGAAGAACTTATTCAAGCTACA 1228

Qy        273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
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Db       1229 AATGGGTTTTCAGCACAAAATTTGTTGGGAGAAGGTGGATTTGGCTGTGTTTATAAAGGT 1288

Qy        293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312

Db       1289 TTGCTGATAGATGGAAGAGAAGTAGCTGTGAAACAGCTCAAAATTGGTGGTGGGCAAGGG 1348

Qy        313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332

Db       1349 GAACGCGAATTCAGGGCAGAAGTTGAGATTATTAGCCGTGTACATCATCGTCATCTGGTT 1408

Qy        333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352

Db       1409 TCTTTAGTTGGTTACTGTATATCCGAGCATCAGAGATTGCTTGTATATGACTATGTTCCC 1468

Qy        353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372

Db       1469 AACGATACTCTTCATTACCATCTCCACGGTGAAAATAGACCAGTTCTAGATTGGCCTACC 1528

Qy        373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392

Db       1529 AGAGTCAAGGTTGCTGCTGGTGCAGCTCGTGGAATAGCTTACTTGCATGAAGACTGTCAT 1588

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412

Db       1589 CCACGCATTATTCATCGAGATATTAAGTCATCAAACATCCTACTTGATCTCAACTATGAA 1648

Qy        413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432

Db       1649 GCTCAAGTTTCGGACTTTGGGCTTGCAAAATTGGCATTAGATTCAAATACACATGTAACT 1708

Qy        433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452

Db       1709 ACACGTGTAATGGGAACCTTTGGGTACATGGCACCAGAATATGCGACAAGTGGAAAACTT 1768

Qy        453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472

Db       1769 ACTGAAAAGTCTGATGTATATTCTTTTGGGGTTGTGCTTTTGGAGCTAATTACAGGTCGG 1828

Qy        473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492

Db       1829 AAGCCTGTAGATGCATCTCAACCAATTGGTGATGAGAGCCTGGTTGAATGGGCTCGACCT 1888

Qy        493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512

Db       1889 CTGTTGACGGAAGCACTTGACAATGAGGACTTTGAAATTTTGGTGGATCCAAGACTGGGG 1948

Qy        513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532

Db       1949 AAGAACTACGATAGAAATGAAATGTTTCGGATGATCGAGGCTGCCGCAGCCTGTGTACGC 2008

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552

Db       2009 CACTCATCGGTGAAGAGACCACGCATGAGTCAGGTGGTGAGAGCTTTAGATTCCTTGGAT 2068

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572

Db       2069 GAGTTTACGGATCTCAATAACGGAATGAAACCGGGACAGAGTTCGGTG------------ 2116

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592

Db       2117 --------------TTTGATTCGGCGCAGCAATCTGCACAAATCAGAATGTTTAGGAGG 2161

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612

Db       2162 ATGGCTTTTGGGAGCCAAGAT------AGTTCCGGTTTCTTCAATGAGTCTCAGAGTAGC 2215

Qy        613 Tyr-GlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMe 632

Db       2216 TGGAGGAGTA----------------------GAGATCACGACCCAACAACTGTCTTC 2251

Qy        632 tGlyLysIleLysArgThrGlyGlnGly 641

Db       2252 TCCCAAAATAAAA---CTGGGCATGGGA 2276
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```
RESULT 14
US-10-425-114-14127
; Sequence 14127, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14127
;   LENGTH: 2190
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB148-034-D5_FLI
US-10-425-114-14127

Alignment Scores:
Pred. No.:              1.09e-84        Length:         2190
Score:                  1437.50         Matches:        331
Percent Similarity:     61.90%          Conservative:   80
Best Local Similarity:  49.85%          Mismatches:     167
Query Match:            41.63%          Indels:         87
DB:                     13              Gaps:           19

US-10-086-464-2 (1-647) x US-10-425-114-14127 (1-2190)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProPro---------------------- 13

Db          2 ATGATGCCTTCTTCCCTCCCTCATTCTCGCTCGCCCCCATTCCACCTTCGACGACCCCTT 61

Qy         14 SerProProSerAsnSerThrThrThrThrProProProAlaSerAlaProPro------ 31

Db         62 TCTCCTTCTCCCTCCTCAATCACCTGCAGCGAAAAGGAAAAGGGTGTCAGACCGTAACTA 121

Qy         31 ------------------------------------------------------------ 31

Db        122 AGAGCTATTTAGCAATAATACATACATAGCTATACCCTCTTTAGGTCAAGAGGGTGGAGT 181

Qy         32 ---ProThrThrProSerSerProProProProSerThrIlePro--------------- 45

Db        182 TCTCCTTATTCGGAGGAAGAGCTCCATCCTCATTCTACAAGACCAAACCAATAAATGGCC 241

Qy         46 ThrSerProProProSerSerArgSerThrProSerAlaProProProSerProProThr 65

Db        242 TCTAGCCCACAGTCCTCGCCATCATCCTCCAAGAAGTCGCCGCCACCACAAGAAGCATCA 301

Qy         66 ProSerThrProGlySerProProProProLeuProGlnProSerProProAlaProThrThr 85

Db        302 GCTTTGGCGCCAAAATCATCTTCA------AAGTCACCCTCGCCACCAAAGGGTGAATCA 355

Qy         86 ProGlySerProProAlaProValThrProProThrArgAsnProProProSerValPro 105

Db        356 ---AATTCATCTCCCAGTCCCCCATCGAAATCGTCCCTGTCACCACCGCCACGACCAAAG 412

Qy        106 GlyProProSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSer 125

Db        413 AAAAGTGCTAGTACATCTAGCTCTAAAGATGGGAAGACGAAGAAGTCGTCTTCATCGTCT 472

Qy        126 ProProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        473 TCATCGTCGGATAATACAGCCGCTGTGATCACCGGCGTGGTGCTTGGGGTG---GTGGGC 529
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Qy      146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165
Db      530 TTCGCTCTGCTCTTGTCCATCGTGGCGTGCGTGTGCTGCGCCAAGAAGAAGAAGAAACGT 589

Qy      166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyPro--------- 182
Db      590 ----------------------------CCGCCCCCAATGAACATGCCCTTCTACACC 619

Qy      183 ---LysAlaGlyGly---------ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGln 198
Db      620 GACGAGAAAGGCAATGTGTATTACCCCAACGCTGGTCTGCCGCCTATGTGGCAGCAATAT 679

Qy      199 AsnAlaThrProProSerAspHisValValThrSerLeuProProProProLysAlaPro 218
Db      680 GGCAGCAAC--------------------GGCAGCATCCCTCCGCCGGG-ATGGCACCA 717

Qy      219 SerProProArgGlnProPro-ProProProProProProPheMetSerSerSerGlyGl 238
Db      718 TCACGGCGGCGGGAACCCGCTGTCGCCATCGCTGGGCTCGATGGCGGCGCCCCTGAGCGG 777

Qy      238 ySerAspTyrSerAsp---------ArgProValLeuProProProSerProGlyLeuVa 255
Db      778 CGAGATGTACTCGTCCGGCCCCCACGGGCCTCCCCTCCCCCCACCTTCGCCGAACGTGGC 837

Qy      255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275
Db      838 GCTGGGGTTCTCCAAGAGCTCCTTCTCGTACGAGGAGCTAGCGGCAGCGACGTCGGGCTT 897

Qy      275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295
Db      898 CTCGTCGGCGAACCTGCTGGGGCAGGGCGGGTTCGGGTACGTGTACAAGGGCGTGCTCGC 957

Qy      295 o---SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluAr 314
Db      958 CGGCAGCGGGAAGGAGGTGGCGGTGAAGCAGCTCAAGTCCGGGAGCGGGCAGGGGGAGCG 1017

Qy      314 gGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLe 334
Db      1018 CGAGTTCCAGGCGGAGGTGGAGATCATCAGCCGCGTGCACCACCGTCACCTGGTGTCGCT 1077

Qy      334 uValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAs 354
Db      1078 CGTGGGCTACTGCATCGCGGGCAACCAGCGCATGCTCGTCTACGAGTTCGTGGCCAACAA 1137

Qy      354 nAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLe 374
Db      1138 CACGCTGGAGCACCATCTGTACGCCAAGGACGGCCCTGTCATGGACTGGAGCACCCGCAT 1197

Qy      374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLy 394
Db      1198 GAAGATCGCGCTCGGCTCCGCCAAGGGCCTCGCCTACCTCCACGAGGACTGCCATCCTCG 1257

Qy      394 sIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLy 414
Db      1258 GATCATCCACCGCGACATCAAGGCCGCCAACATCCTGCTGGACAACAACTTCGAGGCCAT 1317

Qy      414 sValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrAr 434
Db      1318 GGTGGCGGACTTCGGGCTGGCCAAGCTCACGACGGACACCAACACGCACGTCTCCACGCG 1377

Qy      434 gValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGl 454
Db      1378 CGTCATGGGCACCTTCGGCTACCTGGCGCCGGAGTACGCGTCCAGCGGCAAGCTCACGGA 1437

Qy      454 uLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgPr 474
Db      1438 CAGGTCGGACGTCTTCTCCTTCGGCGTCATGCTGCTGGAGCTACTCACGGGGCGCCGCCC 1497

Qy      474 oValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLe 494
Db      1498 CATCGATACCACCAAC---TACATGGAGGACAGCCTCGTGGACTGGGCGCGCCCGCTGCT 1554

Qy      494 uAsnArg------AlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAs 512
Db      1555 GAGCGCCGCGCTGGCGGGGGAGACGGGC---TTCGCCGAGCTCGTCGACCCCCGTCTGGG 1611

Qy      512 nAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValAr 532
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Qy      532 gHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVa 552
Db      1672 CCACTCGGCCAAGCGCCGCCCCAAGATGAGCCAGATCGTGCGCGCGCTGGAGGGCGACGC 1731

Qy      552 lSerLeuSerAspLeuAsn---GluGlyMetArgProGlyGlnSerAsnValTyrSerSe 571
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Qy      571 rTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheAr 591
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Qy      591 gLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSe 611
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Qy      611 rAspTyrGly 614
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RESULT 15
US-10-425-114-6300
; Sequence 6300, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6300
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700560157_FLI
US-10-425-114-6300

Alignment Scores:

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Percent Similarity:	74.27%	Conservative:	45
Best Local Similarity:	64.11%	Mismatches:	80
Query Match:	41.62%	Indels:	34
DB:	13	Gaps:	7

US-10-086-464-2 (1-647) x US-10-425-114-6300 (1-1500)

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Db       11 GGAGGTCCACATGGG---------------------------------------------- 25

Qy      205 AspHisValValThrSerLeuProProProProLysAlaProSerProProArgGlnPro 224
Db       26 GACCATGTTGTG---AGGATGCAACAAAATGGAATGGGTCCTGGTGGCGGAGGGTGGGGT 82

Qy      225 ProProProProProProProPheMetSerSerSerGly------GlySerAspTyrSer 242
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Qy        243 AspArgProVal---LeuProProProSerProGlyLeuValLeuGlyPheSerLysSer 261
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Qy        262 ThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeu 281
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Qy        282 GlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAla 301
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Qy        302 ValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGlu 321
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Qy        322 IleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGly 341
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Qy        342 AlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361
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Qy        422 LysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyr 441
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Qy        442 LeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPhe 461
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Qy        462 GlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyr 481
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Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              |||:::|||      |||   ||||||   :::         ||||||   :::|||:::
Db        920 GGCAACTTTGGAGAGTTGGTTGATGCATTTTTAGAGGGAAACTACGATCCTCAAGAACTG 979

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Db        980 TCAAGAATGGCAGCTTGTGCTGCCGGTAGCATTCGTCATTCTGCCAAAAAACGTCCAAAA 1039

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||   |||||||||:::|||||||||   ||||||   :::|||
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Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Search completed: April 25, 2004, 02:33:32
Job time : 696 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2004, 20:49:18 ; Search time 5877 Seconds
(without alignments)
4771.643 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10086464/runat_11052004_121814_7841/app_query.fasta_1.839
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10086464_@CGN_1_1_5265_@runat_11052004_121814_7841 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	3453	100.0	1944	6	AX825703	AX825703 Sequence
	3	3453	100.0	2189	6	AX825705	AX825705 Sequence
	4	3453	100.0	2189	8	AY028699	AY028699 Brassica
	5	2936.5	85.0	1959	6	AX825738	AX825738 Sequence
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	7	2936.5	85.0	2098	8	AY128792	AY128792 Arabidops
	8	2936.5	85.0	2116	8	AY056788	AY056788 Arabidops
	9	2936.5	85.0	2188	8	AY059901	AY059901 Arabidops
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	22	1746	50.6	2013	8	BT005955	BT005955 Arabidops
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	25	1687	48.9	2025	6	AX825715	AX825715 Sequence
	26	1687	48.9	2104	6	AX088884	AX088884 Sequence
	27	1687	48.9	2104	6	AX825714	AX825714 Sequence
	28	1668	48.3	1515	6	AX825736	AX825736 Sequence
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	36	1479.5	42.8	114367	8	ATF10M10	AL035521 Arabidops
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	38	1479.5	42.8	195921	8	ATCHRIV81	AL161585 Arabidops
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	40	1459.5	42.3	3064	8	AY035076	AY035076 Arabidops
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ALIGNMENTS

RESULT 1

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LOCUS       AX088876               1944 bp    DNA     linear   PAT 17-MAR-2001
DEFINITION  Sequence 1 from Patent WO0114563.
ACCESSION   AX088876
VERSION     AX088876.1  GI:13397639
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
  AUTHORS   Goring,D. and Silva,N.
  TITLE     Proline-rich extensin-like receptor kinases
  JOURNAL   Patent: WO 0114563-A 1 01-MAR-2001;
            Goring, Daphne (CA) ; Silva, Nancy (CA)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              4.02e-76        Length:         1944
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-086-464-2 (1-647) x AX088876 (1-1944)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Db          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Qy        121 ProSerSerProSerProProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
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Db       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
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Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Db       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Db       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2
AX825703
LOCUS       AX825703               1944 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 1 from Patent WO03072763.
ACCESSION   AX825703
VERSION     AX825703.1  GI:39751230
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 1 04-SEP-2003;
            Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES             Location/Qualifiers
     source          1. .1944
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3708"
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                     /codon_start=1
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                     EANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSL
                     VGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCN
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                     KLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLAD
                     AKMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGMRPGQS
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ORIGIN

Alignment Scores:
Pred. No.:              4.02e-76        Length:         1944
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-10-086-464-2 (1-647) x AX825703 (1-1944)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Db          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Db        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Db        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Db        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Db        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Db        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
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Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Db       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941
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RESULT 3
AX825705
LOCUS       AX825705               2189 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 3 from Patent WO03072763.
ACCESSION   AX825705
VERSION     AX825705.1  GI:39751232
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 3 04-SEP-2003;
            Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              4.38e-76        Length:         2189
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

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Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
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Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
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Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
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Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
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Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
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Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
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RESULT 4
AY028699

LOCUS	AY028699 2189 bp mRNA linear PLN 26-MAR-2001
DEFINITION	Brassica napus receptor protein kinase PERK1 mRNA, complete cds.
ACCESSION	AY028699
VERSION	AY028699.1 GI:13447448
KEYWORDS	.
SOURCE	Brassica napus (rape)
ORGANISM	Brassica napus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 2189)
AUTHORS	Silva,N.F. and Goring,D.R.
TITLE	Characterization of a novel Brassica napus receptor protein kinase PERK1
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2189)
AUTHORS	Silva,N.F. and Goring,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (19-MAR-2001) Biology, York University, 4700 Keele Street, Toronto, Ontario M3J 1P3, Canada

FEATURES Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.:	4.38e-76	Length:	2189
Score:	3453.00	Matches:	647
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

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DB:                 8          Gaps:          0

US-10-086-464-2 (1-647) x AY028699 (1-2189)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Db        277 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 336

Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
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Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
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Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
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Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
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Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
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RESULT 5
AX825738
LOCUS       AX825738               1959 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 36 from Patent WO03072763.
ACCESSION   AX825738
VERSION     AX825738.1  GI:39751255
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 36 04-SEP-2003;
            Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES             Location/Qualifiers
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Best Local Similarity:    86.97%        Mismatches:      41
Query Match:              85.04%        Indels:          21
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US-10-086-464-2 (1-647) x AX825738 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
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Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Db        343 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 399

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Db        697 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 756

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Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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Db        877 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 936

Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Db        937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 996

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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Db        997 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1056

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
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Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
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Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
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Db       1177 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1236

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Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
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BT008400
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DEFINITION  Arabidopsis thaliana At3g24550 gene, complete cds.
ACCESSION   BT008400
VERSION     BT008400.1  GI:30725473
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
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            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     The discrepancy does not affect the protein sequence.
            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
            Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J.,
            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
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Score:                  2936.50         Matches:        574
Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x BT008400 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db          1 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 60

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db         61 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 120

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
Db        757 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 816

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
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Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
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Db       1777 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1836

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Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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RESULT 7
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VERSION AY128792.1 GI:22136227
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2098)
AUTHORS Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Tripp,M., Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Tripp,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES Location/Qualifiers
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ORIGIN

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Pred. No.:              1.29e-63        Length:         2098
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Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x AY128792 (1-2098)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::|||||||||||||||||||||||||||||||||||||      |||:::|||
Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

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Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Db        817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 876

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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VERSION     AY056788.1  GI:15983764
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  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
            Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis cDNA clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2116)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
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            Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
            Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L.,
            Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
            Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
            Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
            Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S.,
            Davis,R.W.,  Theologis,A., and Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
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ORIGIN

Alignment Scores:
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Score:                  2936.50         Matches:        574
Percent Similarity:     90.61%          Conservative:   24
Best Local Similarity:  86.97%          Mismatches:     41
Query Match:            85.04%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x AY056788 (1-2116)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db         37 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 96

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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REFERENCE   1  (bases 1 to 2188)
  AUTHORS   Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2001) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
            Southwick,A., Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
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ORIGIN

Alignment Scores:
Pred. No.:              1.33e-63        Length:         2188
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US-10-086-464-2 (1-647) x AY059901 (1-2188)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db         32 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 91

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
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Db        788 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 847

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Db        848 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 907

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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RESULT 10
AY093065

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REFERENCE   1  (bases 1 to 2190)
  AUTHORS   Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Southwick,A.,
            Nguyen,M., Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
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ORIGIN
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Alignment Scores:

Pred. No.:	1.33e-63	Length:	2190
Score:	2936.50	Matches:	574
Percent Similarity:	90.61%	Conservative:	24
Best Local Similarity:	86.97%	Mismatches:	41
Query Match:	85.04%	Indels:	21
DB:	8	Gaps:	12

US-10-086-464-2 (1-647) x AY093065 (1-2190)

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Db       1566 GATTCAAAGATGGGTAATGAGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1625

Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
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Db       1626 GCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1685

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
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Db       1686 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1745

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
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Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
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Db       1806 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1865

Qy        608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
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Db       1866 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1925

Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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BT008409
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DEFINITION  Arabidopsis thaliana At3g24600 gene, complete cds.
ACCESSION   BT008409
VERSION     BT008409.1  GI:30725491
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
            Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J.,
            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     YAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEEGDF
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ORIGIN

Alignment Scores:
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Score:                  2934.50         Matches:        573
Percent Similarity:     90.61%          Conservative:   25
Best Local Similarity:  86.82%          Mismatches:     41
Query Match:            84.98%          Indels:         21
DB:                     8               Gaps:           12

US-10-086-464-2 (1-647) x BT008409 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Db          1 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 60

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Db         61 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 120

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||
Db        121 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 180

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
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Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Db        580 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 639

Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
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Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
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Db        757 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 816

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Db        817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 876

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
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Db        877 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 936

Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
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Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
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Db        997 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1056

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
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Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
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Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
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Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Db       1297 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1356

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
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Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
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Db       1417 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1476

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RESULT 12
AF370509
LOCUS AF370509 2257 bp mRNA linear PLN 30-APR-2001
DEFINITION Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA, complete cds.
ACCESSION AF370509
VERSION AF370509.1 GI:13877616
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2257)
AUTHORS Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
TITLE Direct Submission
JOURNAL Submitted (17-APR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Southwick,A. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

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ORIGIN

Alignment Scores:

| | | | |
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| Pred. No.: | 1.52e-63 | Length: | 2257 |
| Score: | 2934.50 | Matches: | 573 |
| Percent Similarity: | 90.61% | Conservative: | 25 |
| Best Local Similarity: | 86.82% | Mismatches: | 41 |
| Query Match: | 84.98% | Indels: | 21 |
| DB: | 8 | Gaps: | 12 |

US-10-086-464-2 (1-647) x AF370509 (1-2257)

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Qy   1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy   18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
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Db   167 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 226

Qy   36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
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Qy   55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy   75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
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Db   335 ATTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 391

Qy   95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Qy   114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Qy   132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db   506 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 565

Qy   152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
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Qy   170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Db        746 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 802

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Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267

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Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347

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Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387

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Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447

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Db       1463 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1522

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Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527

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RESULT 13
AY089024

LOCUS	AY089024 2324 bp mRNA linear PLN 14-APR-2003
DEFINITION	Arabidopsis thaliana clone 17909 mRNA, complete sequence.
ACCESSION	AY089024
VERSION	AY089024.1 GI:21407798
KEYWORDS	FLI_CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 2324)
AUTHORS	Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE	Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE	22088475
PUBMED	12093376
REFERENCE	2 (bases 1 to 2324)
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Full-Length cDNA from Arabidopsis thaliana
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 2324)
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Direct Submission
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/clone="17909"

ORIGIN

Alignment Scores:			
Pred. No.:	2.45e-62	Length:	2324
Score:	2885.00	Matches:	570
Percent Similarity:	90.30%	Conservative:	26
Best Local Similarity:	86.36%	Mismatches:	42

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Query Match:          83.55%      Indels:        23
DB:                   8           Gaps:          13

US-10-086-464-2 (1-647) x AY089024 (1-2324)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
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Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db        165 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 224

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||    |||||||||      ||||||||||||||||||||||
Db        225 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 284

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
                 ||||||   ||||||||||||||||||      |||           ||||||
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
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Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||         |||:::||||||              |||||||||:::   ||||||
Db        390 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 446

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
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Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db        504 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 563

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Db        564 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 623

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
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Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
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Db        681 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 740

Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
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RESULT 14
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ACCESSION   AB020746 BA000014
VERSION     AB020746.1  GI:3985949
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SOURCE      Arabidopsis thaliana (thale cress)
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 3. II.
            Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
            and BAC clones
  JOURNAL   DNA Res. 7 (3), 217-221 (2000)
  MEDLINE   20363099
   PUBMED   10907853
REFERENCE   2  (bases 1 to 79706)
  AUTHORS   Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOB24
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
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            The 5' clone is MXP5 and the 3' clone is MSD24.
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                CISPTHLGISFKQSCISSRVKAHISRISKEVPNLFEIITEPSPHALVVKGLKKIGIMI
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Score:                  2622.00         Matches:        573
Percent Similarity:     61.19%          Conservative:   23
Best Local Similarity:  58.83%          Mismatches:     43
Query Match:            75.93%          Indels:         337
DB:                     8               Gaps:           19

US-10-086-464-2 (1-647) x AB020746 (1-79706)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
              ||||||:::||||||||||||||||||          ||||||||||||||||||:::
Db      51787 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 51846

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db      51847 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 51906

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||
Db      51907 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 51966

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
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Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
Db      52015 CTTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 52071

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
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Db      52072 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 52128

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
                 |||   :::||||||   ||||||:::       ||||||||||||||   ||||||
Db      52129 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 52185

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
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Db      52186 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 52245

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::|||||||||||||||||||||||||||||||||||||      |||:::|||
Db      52246 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 52305

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAla---------------- 184
                 ||||||||||||||||||||||||||||   |||||||||
Db      52306 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGG-TAAATTCAAAGATCT 52364

Qy        184 ------------------------------------------------------------ 184

Db      52365 CAACTTCATGAAATAAAAATCGAATATTTAACCATAGTTGTTCAATTCTGATACGAATTG 52424

Qy        184 ------------------------------------------------------------ 184

Db      52425 CTCAAATCTGATACTTGATTATGCATTGTTATCTGTTAAAGAGATTACCTTTGTGGAAAA 52484

Qy        185 -------------------------------------GlyGlyProTyrGlyGlyGln 191
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Db      52485 GTTTCAAACTTTACAGAGATTTGATGTTGTTTATCAGCTGGAGGACCTTACGGTGGTCAA 52544

Qy        192 GlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValValThrSer 210
              ||||||   |||:::|||||||||||:::   |||||||||   ||||||||||||||||
Db      52545 CAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTGACGTCA 52604

Qy        211 LeuProProProProLysAlaProSerProProArgGlnProProProProProProPro 230
              |||   ||||||||||||   ||||||||||||||:::||||||||||||||||||||
Db      52605 TTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCTCCACCA 52661

Qy        231 Pro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProPro 249
              |||   ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db      52662 CCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTTCCTCCA 52721

Qy        250 ProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla 269
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Db      52722 CCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAGTTGTCG 52781

Qy        270 ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrVal 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52782 AGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGTTATGTG 52841

Qy        290 HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer 309
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Db      52842 CATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCTGGTAGT 52901

Qy        310 GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg 329
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Db      52902 GGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCATCACAGG 52961

Qy        330 HisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGlu 349
              ||||||||||||||:::||||||||:::||||||   :::||||||||||||||||||||
Db      52962 CATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTCTATGAG 53021

Qy        350 PheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGlu----------------- 363
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Db      53022 TTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTTA-GAACAAAACTAAACTCTT 53080
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Qy        363 ------------------------------------------------------------ 363

Db      53081 TCTTTTGATTTTGTTACATTGCTTTGTTGTTTTCAGTTAGTGATGATTTGTTTGGGAATT 53140

Qy        364 ------------------GlyArgProThrMetGluTrpSerThrArgLeuLysIleAla 377
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Db      53141 GAATTTGTTATAGGTAAGGGACGGCCTACGATGGAATGGAGTACTAGATTGAAGATTGCT 53200

Qy        378 LeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys------------------ 391
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Db      53201 CTTGGATCTGCTAAAGGACTTTCATATCTTCATGAAGATTGTAAGTCTAAAACCTTAAAA 53260

Qy        391 ------------------------------------------------------------ 391

Db      53261 ATTATGTACAGATGTTTGATAAATACTGTCTTTGTTTGTCACTGAGGTATATATATAAAT 53320

Qy        392 ----------AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAs 408
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Db      53321 ATTTGCAGGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATTGA 53380

Qy        408 pPheLysPheGluAlaLys------------------------------------------ 414
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Db      53381 TTTCAAATTTGAAGCTAAGGTATGTTTACTCGATATGTTTTGTGAAGTGTTTTTGTAATT 53440

Qy        415 ----------------------------ValAlaAspPheGlyLeuAlaLysIleAlaS 425
                                           ||||||||||||||||||||||||||||||
Db      53441 TGTGTCACTAAAGCTCTTCTTTCTTTCAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTT 53500

Qy        425 erAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly------------- 440
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Db      53501 CTGATACAAACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTAAAAATCATCTT 53560

Qy        440 ------------------------------------------------------------ 440

Db      53561 TAATCTACTAAACATGTACATTTATGCAGTTTGCTTAATGCATGTGATCCTTGTGCAACA 53620

Qy        441 --------------------------------TyrLeuAlaProGluTyrAlaAlaSerG 450
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Db      53621 AGTTCTGAAACTTTTGGTTTTGGGATTTTAGGTATTTGGCTCCGGAATATGCTGCAAGTG 53680

Qy        450 lyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleT 470
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Db      53681 GAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAACTTATTA 53740

Qy        470 hrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp- 489
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Db      53741 CTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTTGACTGGG 53800

Qy        489 ------------------------------------------------------------ 489

Db      53801 TACTTTACTATGACTGCAGATAATCTAAACTTCTGATTTTTCTACAATTTAACTGTTGAC 53860

Qy        490 ----------------------------------AlaArgProLeuLeuAsnArgAla 497
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Db      53861 TAAAGCAAAAGCTATGTGTGATTGATGGTGGAACAGGCACGACCATTGCTTAACCGAGCA 53920

Qy        498 SerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArg 517
                ||||||:::|||||||||||||||||||||||:::||||||   |||   |||||||||
Db      53921 TCTGAGGAAGGAGATTTTGAGGGTTTGGCTGATTCAAAGATGGGTAATGAGTATGACAGA 53980

Qy        518 GluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArg 537
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Db      53981 GAGGAGATGGCTCGCATGGTTGCTTGCGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGC 54040

Qy        538 ArgProArgMetSer---------------------------------------------- 542
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Db      54041 AGACCTCGCATGAGCCAGGTAACTTAATCCTTTTCTCTAGAGAAGAGCATATTGGTTTGG 54100

Qy        542 ------------------------------------------------------------ 542

Db      54101 TTCTGTTTATTTGGTAGAATAATATGTTTCCGTATGGTTTTAAAGAAAGGTTTTGATATG 54160

Qy        542 ------------------------------------------------------------ 542

Db      54161 GTTTTTGTGAGAAAGATCGGTTCAGTTATGTTCTTATGCCTAGCCCTACTTTTTGTTACC 54220

Qy        542 ------------------------------------------------------------ 542

Db      54221 CATCATCATACTATCTAAACAACACCGATTGAATATGTCAAAAGAATTGGCTGCAGTTTC 54280

Qy        542 ------------------------------------------------------------ 542

Db      54281 TTTTGTTTTCATTTTGCCAAGGATTGTCATTTTAACATATGTTAATGCTAATGGAGTGAG 54340

Qy        543 ---------------------GlnIleValArgAlaLeuGluGlyAsnValSerLeuSer 555
                                    ||||||||||||||||||||||||||||||||||||||
Db      54341 TGATTTGCTGTACAAAATGAGCAGATAGTACGGGCGTTAGAAGGAAATGTATCGCTGTCT 54400

Qy        556 AspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySer 575
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Db      54401 GATCTTAACGAAGGGATGAGACCGGGTCACAGCAACGTATACAGCTCATATGGAGGAAGC 54460

Qy        576 ThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeu 595
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Db      54461 ACAGACTATGACACGAGCCAATACAACGACGACATGATAAAGTTTAGGAAAATGGCTCTT 54520

Qy        596 GlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeu 615
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Db      54521 GGAACTCAAGAATACGGCACAACCGGCGAGTACAGTAATCCAACCAGTGACTACGGACTG 54580

Qy        616 TyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIle 635
                |||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db      54581 TACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACACGAGAAATGGAGATGGGAAAGATT 54640

Qy        636 LysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
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RESULT 15
AK103247
LOCUS       AK103247               2307 bp    mRNA    linear   PLN 24-JUL-2003
DEFINITION  Oryza sativa (japonica cultivar-group) cDNA clone:J033123K23, full
            insert sequence.
ACCESSION   AK103247
VERSION     AK103247.1  GI:32988456
KEYWORDS    FLI_CDNA; CAP trapper.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   The Rice Full-Length cDNA Consortium, National Institute of
            Agrobiological Sciences Rice Full-Length cDNA Project Team:,
            Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
            Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
            Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
            Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
            Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
            Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
            Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
            Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
            Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
            Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:,
            Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
            Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
            Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
            Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
            Yoshino,M. and Hayashizaki,Y.
  TITLE     Collection, mapping, and annotation of over 28,000 cDNA clones from
            japonica rice
  JOURNAL   Science 301 (5631), 376-379 (2003)
  MEDLINE   22752273
   PUBMED   12869764
REFERENCE   2  (bases 1 to 2307)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
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Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

TITLE Direct Submission

JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES Location/Qualifiers
source 1. .2307
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033123K23"

ORIGIN

Alignment Scores:

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Percent Similarity:	64.39%	Conservative:	75
Best Local Similarity:	53.91%	Mismatches:	138
Query Match:	53.33%	Indels:	117
DB:	8	Gaps:	18

US-10-086-464-2 (1-647) x AK103247 (1-2307)

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Qy        3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22
            ::::::|||          ||||||                        :::|||::::::
Db        7 GCGTCGCCAGTAGACTCCACTGGGGACGGTGTGGGTGGTGGTGGTAGTAGTAGTTCTCGC 66

Qy       23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42
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Qy       43 ThrIleProThrSerProProProSerSerArg-------------------------- 53
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Db      109 ------------TCACCACCGCCGCGAGGGAGAAAAAGCTCTTGCCTGCTCTTTTCTTGG 156

Qy       53 ---------------------------------------------------------- 53

Db      157 CTCCGCTTTGTTCTTGCTCTCATCTTGCTCGTGGCGTGGTAGTCTTCGACTCGTTCTTTT 216

Qy       53 ---------------------------------------------------------- 53

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Qy      164 ArgArgArgAspGluGluAspAla--------------------------TyrTyr--- 173
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Qy      212 ProProProProLysAlaProSerProProArgGlnProProProProProProPro 231
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Db      766 ---------AAGAAGGTGCCTTCGCATCCTTCCCCTCCACCACCTCCTGCTCCACTAAAT 816

Qy      232 PheMetSerSerSerGlySerAspTyrSer------------AspArgProValLeu 247
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Qy      268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
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Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Search completed: May 13, 2004, 00:33:01

Job time : 5986 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2004, 20:46:26 ; Search time 603 Seconds
(without alignments)
4558.183 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	3453	100.0	1944	9	ACF36548	Acf36548 B. napus
3	3453	100.0	2189	9	ACF36549	Acf36549 B. napus
4	2936.5	85.0	1959	9	ACF36557	Acf36557 A. thalia
5	2885	83.6	2324	3	AAC36968	Aac36968 Arabidops
6	1821.5	52.8	1812	9	ACF36554	Acf36554 O. sativa
7	1668	48.3	1515	9	ACF36555	Acf36555 Z. mays P
8	1637.5	47.4	1488	9	ACF36556	Acf36556 G. max PE
9	1507	43.6	2520	4	AAF77096	Aaf77096 Arabidops
10	1504	43.6	2520	9	ACF36551	Acf36551 Arabidops
11	1479.5	42.8	2820	4	AAF77097	Aaf77097 Arabidops
12	1471.5	42.6	2820	9	ACF36552	Acf36552 Arabidops
13	1209.5	35.0	2880	4	AAF77095	Aaf77095 Arabidops
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16	1181	34.2	3060	4	AAF77098	Aaf77098 Arabidops
17	839.5	24.3	1923	7	ADA70890	Ada70890 Rice gene
18	816.5	23.6	2124	6	ABZ13274	Abz13274 Arabidops
19	804.5	23.3	2865	7	ADA70701	Ada70701 Rice gene
20	802.5	23.2	2011	4	AAH22557	Aah22557 P. patens
21	797	23.1	1730	7	ADA70647	Ada70647 Rice gene
22	793.5	23.0	2823	7	ADA69478	Ada69478 Rice gene
23	782.5	22.7	1419	3	AAC43029	Aac43029 Arabidops
24	782.5	22.7	1419	6	ABZ13121	Abz13121 Arabidops
25	775.5	22.5	1626	3	AAC48313	Aac48313 Arabidops
26	775.5	22.5	1917	7	ADA70527	Ada70527 Rice gene
27	773	22.4	1479	3	AAC43040	Aac43040 Arabidops
28	769.5	22.3	1353	3	AAC42860	Aac42860 Arabidops
29	769.5	22.3	1353	6	ABZ14106	Abz14106 Arabidops
30	766	22.2	1494	3	AAC48560	Aac48560 Arabidops
31	758.5	22.0	1572	3	AAC42898	Aac42898 Arabidops
32	758.5	22.0	1572	6	ABZ13705	Abz13705 Arabidops
33	758.5	22.0	1920	6	AAL45905	Aal45905 A thalian
34	758.5	22.0	2012	3	AAC44847	Aac44847 Arabidops
35	756	21.9	3239	3	AAA79271	Aaa79271 Eucalyptu
36	754.5	21.9	2136	7	ADA69829	Ada69829 Rice gene
37	749.5	21.7	1751	3	AAC45313	Aac45313 Arabidops
38	744.5	21.6	1485	3	AAC42702	Aac42702 Arabidops
39	740.5	21.4	3525	7	ADA71170	Ada71170 Rice gene
40	740	21.4	2868	3	AAA79266	Aaa79266 Pinus rad
41	740	21.4	3153	7	ADA71066	Ada71066 Rice gene
42	736.5	21.3	1703	3	AAC46629	Aac46629 Zea mays
43	736	21.3	3624	7	ADA69512	Ada69512 Rice gene
44	735	21.3	2004	3	AAC40780	Aac40780 Arabidops
45	734	21.3	1455	3	AAC45877	Aac45877 Arabidops

ALIGNMENTS

RESULT 1
AAF77094
ID AAF77094 standard; DNA; 1944 BP.
XX
AC AAF77094;
XX
DT 17-MAY-2001 (first entry)
XX
DE Brassica napus PERK1 DNA.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Brassica napus.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,

PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Claim 6; Fig 1; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.62e-93	Length:	1944
Score:	3453.00	Matches:	647
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-086-464-2 (1-647) x AAF77094 (1-1944)

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Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Db        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
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Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

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Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

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Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

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Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
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Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
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Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
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Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
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Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2
ACF36548
ID   ACF36548 standard; cDNA; 1944 BP.
XX
AC   ACF36548;
XX
DT   18-DEC-2003  (first entry)
XX
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "PERK1"
FT                   /note= "Proline-rich Extensin-like Receptor Kinase"
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PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Claim 3; Fig 1A; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.62e-93        Length:         1944
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-086-464-2 (1-647) x ACF36548 (1-1944)

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Qy         21 ThrThrThrProProProAlaSerAlaProProThrThrProSerSerProProPro 40
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Db         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
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Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
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Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
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Db        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
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Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
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Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

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Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
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Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
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Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
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Db        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
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Db        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
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Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

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Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360

Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380

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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440

Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460

Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480

Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500

Db       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520

Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540

Db       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560

Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580

Db       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600

Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620

Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640

Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647

Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 3
ACF36549
ID   ACF36549 standard; cDNA; 2189 BP.
XX
AC   ACF36549;
XX
DT   18-DEC-2003  (first entry)
XX
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
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FT                   /note= "ABR82938; this protein contains the amino acids
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FT                   relevant aa residues (ABR82937) is used in the invention"
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XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937, ABR82938.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 1D; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5e-93          Length:        2189
Score:                  3453.00        Matches:       647
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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     9              Gaps:          0

US-10-086-464-2 (1-647) x ACF36549 (1-2189)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
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Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
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Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
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Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
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Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
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Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
              ||||||||||||||||||||||
Db       2017 GGTTATAGTGGACCTTCTCTT 2037

RESULT 4
ACF36557
ID   ACF36557 standard; DNA; 1959 BP.
XX
AC   ACF36557;
XX
DT   18-DEC-2003  (first entry)
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XX
DE   A. thaliana PERK1 protein encoding genomic DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D, Silva N, Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21d; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents an A. thaliana PERK1 DNA (At3g24550)
XX
SQ   Sequence 1959 BP; 496 A; 514 C; 425 G; 524 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                5.28e-78        Length:          1959
Score:                    2936.50         Matches:         574
Percent Similarity:       90.61%          Conservative:    24
Best Local Similarity:    86.97%          Mismatches:      41
Query Match:              85.04%          Indels:          21
DB:                       9               Gaps:            12

US-10-086-464-2 (1-647) x ACF36557 (1-1959)

Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
              ||||||:::|||||||||||||||||||          |||||||||||||||||||:::
Db          1 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 60

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db         61 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 120

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||||
Db        121 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 180

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              ||||||   ||||||||||||||||||          |||                ||||||
Db        181 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT------------CCTCCT 228

Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||    ||||||   ||||||   |||||||||:::|||   |||
Db        229 CTTCCTCAACCTTCCCCCTCCGCTCCCATCACTCCT---TCTCCACCGTCTCCCACCACA 285

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||         |||:::||||||          |||||||||:::   ||||||
Db        286 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 342

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
                 |||   :::||||||   ||||||:::      ||||||||||||||   ||||||
Db        343 ---GGATCTACTCCTAGAACTCCATCAAACACTAAACCGTCGCCGCCGTCTGATTCTTCC 399

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        400 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 459

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::||||||||||||||||||||||||||||||||||||||      |||:::|||
Db        460 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 519

Qy        170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
                ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        520 GCTGCTTACTATGTTCCTCCTCCTCCTCCATCTGGTCCCAAAGCTGGAGGACCTTACGGT 579

Qy        190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
              ||||||||||||    |||:::||||||||||:::   |||||||||   |||||||||
Db        580 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 639

Qy        209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
              |||||||||   ||||||||||||   ||||||||||||||:::|||||||||||||||
Db        640 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 696

Qy        229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
              |||||||||   ||||||||||||||||||||||||||||||||||   |||||||||
Db        697 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 756

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCTAAAAGCACTTTCACTTATGAGGAG 816

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TTGTCGAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 876

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        877 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 936

Qy        308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GGTAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 996

Qy        328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
              ||||||||||||||||||||:::||||||||:::||||||   :::||||||||||||
Db        997 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCCGGTGTTCAAAGATTACTTGTC 1056

Qy        348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
              ||||||||||||||||||||||||||||||   ||||||||||:::|||||||||||||
Db       1057 TATGAGTTTGTTCCAAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGACGGCCTACG 1116

Qy        368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1176

Qy        388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1236

Qy        408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAAGATTGCTTCTGATACA 1296

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCGGAATATGCT 1356

Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuGluLeu 467
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GCAAGTGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTACTTTTGGAA 1416

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 CTTATTACTGGGAGGCGCCCTGTTGATGCGAACAATGTCTATGTAGATGACAGCTTAGTT 1476

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
                ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1477 GACTGGGCACGACCATTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGAGGGTTTGGCT 1536

Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
                |||:::||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db       1537 GATTCAAAGATGGGTAATGAGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1596

Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1656

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
                ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       1657 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1716

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
                ||||||||||||||||||||||||||||||||||:::||||||||||||:::||||||
Db       1717 GTATACAGCTCATATGGAGGAAGCACAGACTATGACACGAGCCAATACAACGACGACATG 1776

Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
                  ||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db       1777 ATAAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1836

Qy        608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db       1837 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1896

Qy        628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
                ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       1897 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 1956
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RESULT 5
AAC36968
ID AAC36968 standard; DNA; 2324 BP.
XX
AC AAC36968;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15710.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
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PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139458P.
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PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 16-SEP-1999; 99US-0154039P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.:	1.88e-76	Length:	2324
Score:	2885.00	Matches:	570
Percent Similarity:	90.30%	Conservative:	26
Best Local Similarity:	86.36%	Mismatches:	42
Query Match:	83.55%	Indels:	23
DB:	3	Gaps:	13

US-10-086-464-2 (1-647) x AAC36968 (1-2324)

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Qy          1 MetSerSerAlaProSerProGlyThr---------GlySerProProSerProProSer 17
              ||||||:::||||||||||||||||||          ||||||||||||||||||:::
Db        105 ATGTCCACAGCGCCGTCTCCAGGCACTACTCCATCACCATCTCCACCGTCTCCTCCCACA 164

Qy         18 AsnSerThrThrThrThrProProProAla------SerAlaProProProThrThrPro 35
              ||||||||||||||||||||||||||||||      |||   ||||||   |||||||||
Db        165 AACTCGACAACCACCACTCCTCCTCCAGCAGCCTCTTCTCCTCCTCCCACCACAACTCCT 224

Qy         36 SerSerProProPro---ProSerThrIleProThrSerProProProSerSerArgSer 54
              ||||||||||||||   |||||||||      ||||||||||||||||||||
Db        225 TCTTCTCCTCCTCCGTCGCCGTCAACTAATTCAACCTCTCCTCCTCCTTCTTCTCCTTTA 284

Qy         55 ThrProSerAlaProProProSerProProThrProSerThrProGlySerProProPro 74
              ||||||   ||||||||||||||||||          |||             ||||||
Db        285 CCTCCTTCTCTTCCTCCTCCATCTCCTCCTGGATCTTTAACT-----------CCTCCT 332

Qy         75 LeuProGlnProSerProProAlaProThrThrProGlySerProProAlaProValThr 94
              ||||||||||||||||||   ||||||   ||||||   |||||||||:::|||   |||
Db        333 CTTCCTCAACCTTCTCCATCCGCTCCCATCACTCCT---TCCCCGCCGTCTCCCACCACA 389

Qy         95 ProProThr---ArgAsnProProProSerValProGlyProProSerAsnProSerArg 113
              |||         |||:::||||||          |||||||||:::   ||||||
Db        390 CCCTCAAACCCTCGAAGCCCTCCATCTCCTAACCAAGGACCACCAAACACTCCCTCA--- 446

Qy        114 GluGlyGlySerProArgProProSerSer------ProSerProProSerProSerSer 131
              |||   :::||||||   ||||||:::       ||||||||||||||   ||||||
Db        447 ---GGATCTACTCCTAGAACTCCATCAAACGCTAAACCGTCGCCACCGTCTGATTCTTCC 503

Qy        132 AspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuVal 151
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        504 GATGGATTGTCTACCGGAGTTGTGGTAGGAATCGCCATTGGAGGAGTCGCTATTCTTGTT 563

Qy        152 IleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg------AspGluGlu 169
              |||:::|||||||||||||||||||||||||||||||||||||      |||:::|||
Db        564 ATACTGACTCTGATTTGTCTTCTCTGTAAGAAGAAACGAAGAAGAAGACACGACGATGAA 623
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Qy       170 AspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTyrGly 189
Db       624 GCTGCTTACTATGTT---CCTCCTCCTCCTTCTGGTCCCAAAGCTGGAGGACCTTACGGT 680

Qy       190 GlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp---HisValVal 208
Db       681 GGTCAACAACAGTATTGGCAACAACAAAACGCGTCACGGCCGTCAGATAATCATGTAGTG 740

Qy       209 ThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPro 228
Db       741 ACGTCATTG---CCACCACCTAAGCCTCCATCTCCACCACGAAAACCTCCTCCGCCACCT 797

Qy       229 ProProPro---PheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeu 247
Db       798 CCACCACCAGCATTCATGAGTAGCAGTGGTGGTTCTGACTATTCGGATCTTCCGGTTCTT 857

Qy       248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
Db       858 CCTCCACCATCTCCAGGGCTTGTGTTAGGCTTTTCAAAAAGCACTTTCACTTATGAGGAG 917

Qy       268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
Db       918 TTGTCAAGAGCTACTAATGGCTTCTCTGAGGCTAATTTGTTAGGACAAGGAGGGTTTGGT 977

Qy       288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
Db       978 TATGTGCATAAAGGTATATTGCCTAGTGGGAAAGAAGTTGCTGTGAAACAGTTGAAAGCT 1037

Qy       308 GlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHis 327
Db      1038 GGGAGTGGTCAGGGAGAGAGAGAGTTTCAGGCTGAGGTTGAGATCATTAGCAGAGTTCAT 1097

Qy       328 HisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuVal 347
Db      1098 CACAGGCATTTGGTTTCTCTTATTGGTTATTGTATGGCTGATGTTCAAAGATTGCTTGTC 1157

Qy       348 TyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThr 367
Db      1158 TATGAGTTTGTTCCTAACAACAATCTTGAGTTTCACCTCCATGGTAAGGGAAGGCCTACA 1217

Qy       368 MetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeu 387
Db      1218 ATGGAATGGAGTACTAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCATATCTT 1277

Qy       388 HisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIle 407
Db      1278 CATGAAGATTGCAATCCGAAAATCATTCACCGTGATATTAAGGCGTCAAACATATTGATT 1337

Qy       408 AspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThr 427
Db      1338 GATTTCAAATTTGAAGCTAAGGTTGCTGACTTTGGTCTTGCCAGGATTGCTTCTGATACA 1397

Qy       428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
Db      1398 AACACTCATGTATCTACACGCGTGATGGGAACCTTTGGGTATTTGGCTCCAGAATATGCT 1457

Qy       448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
Db      1458 GCAAGCGGAAAGCTCACAGAAAAGTCTGACGTTTTCTCATTTGGTGTTGTACTTTTGGAG 1517

Qy       468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
Db      1518 CTTATAACCGGGAGGCGCCCTGTTGATGCAAACAATGTCTATGTAGATGACAGCTTAGTT 1577

Qy       488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
Db      1578 GACTGGGCACGACCCTTGCTTAACCGAGCATCTGAGGAAGGAGATTTTGATGGTTTGGCT 1637

Qy       508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
Db      1638 GATTCAAAGATGGGTAATGAGTATAG-AGAGAGGAGATGGCTCGCATGGTTGCTTGCGCT 1696

Qy       528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
Db      1697 GCAGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATAGTACGGGCG 1756

Qy       548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
Db      1757 TTAGAAGGAAATGTATCGCTGTCTGATCTTAACGAAGGGATGAGACCGGGTCACAGCAAC 1816

Qy       568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMet 587
Db      1817 GTATACAGCTCATATGGAGGAAGCACTGACTATGACACGAGCCAATACAACGATGACATG 1876

Qy       588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSer 607
Db      1877 AAGAAGTTTAGGAAAATGGCTCTTGGAACTCAAGAATACGGCACAACCGGCGAGTACAGT 1936

Qy       608 AsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThr 627
Db      1937 AATCCAACCAGTGACTACGGACTGTACCCGTCTGGTTCAAGCAGTGAAGGTCAAGCCACA 1996

Qy       628 ArgGluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
Db      1997 CGAGAAATGGAGATGGGAAAGATTAAGAAAACCGGTCAAGGTTATAGTGGACCCTCTCTT 2056
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RESULT 6
ACF36554
ID   ACF36554 standard; DNA; 1812 BP.
XX
AC   ACF36554;
XX
DT   18-DEC-2003 (first entry)
XX
DE   O. sativa PERK protein encoding genomic DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; rice; gene;
KW   ds.
XX
OS   Oryza sativa.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D, Silva N, Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21a; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be

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CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents an O. sativa PERK protein encoding genomic DNA (TIGR
CC   Accession No. TC102111)
XX
SQ   Sequence 1812 BP; 409 A; 487 C; 512 G; 404 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.6e-45       Length:          1812
Score:                  1821.50       Matches:         370
Percent Similarity:     71.62%        Conservative:    69
Best Local Similarity:  60.36%        Mismatches:      119
Query Match:            52.75%        Indels:          55
DB:                     9             Gaps:            15

US-10-086-464-2 (1-647) x ACF36554 (1-1812)

Qy         54 SerThrProSerAlaProProProSerProProThrProSerThrProGlySerProPro 73
              |||:::||||||:::|||||||||:::      |||               :::||||||
Db          4 TCGTCGCCGTCGTCGCCGCCGCCGGCTAACCAGACG-----------GCGACACCGCCT 51

Qy         74 ProLeuProGlnProSer------ProProAlaProThrThrProGlySerProProAla 91
              |||      |||   :::      |||||||||                  ||||||||||||
Db         52 CCGGCTAACCAGACGGCGGCGCCACCTCCGGCGAGCAACAACTCGTCGTCGCCGCCGGCG 111

Qy         92 Pro------ValThrProProThrArgAsnProProProSerValProGlyProProSer 109
              |||      ::::::||||||:::         ||||||:::   |||   |||||||||
Db        112 CCGGGCTCTTTGTCTCCGCCCTCGCTGACG---CCTCCCGCAGCGCCATCGCCTCCGTCG 168

Qy        110 AsnProSerArgGluGlyGlySerProArgProProSerSerPro---SerProProSer 128
                                                 ||||||||||||   :::      :::
Db        169 ACC--------------------------ACGCCCTCCTCGCCGGCGGCGGCGGCGGCG 201

Qy        129 ProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAla 148
              ||||||   |||||||:::|||   ||||||||||||||   :::||||||:::
Db        202 GCGTCGAGCTCGGGGCTGACGACGCCCGTGGTGGTGGGGATCGTGGTGGGCGGCCTCGTC 261

Qy        149 LeuLeuValIleValThr------LeuIleCysLeuLeuCysLysLysLysArgArgArg 166
              :::|||::::::||||||      |||:::||||||      ||||||||||||
Db        262 GTGCTGCTGCTCGTCACCATCCTGCTCGTCTGCCTGTTCAAGAAGAAGAAGCGGCACCAC 321

Qy        167 AspGluGluAspAla-------------------------TyrTyr---------Val 174
                                                      ||||||
Db        322 CACCACCACCCTCCGCCGCCGCCGCCGCCGCACCTCCTGCACTACTACGGCCACCCGCCG 381

Qy        175 ProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGln 194
              ||||||||||||||||||   |||      |||      |||||||||      |||
Db        382 CCGCCGCCGCCGCCCCCGCCGCCGTTCAAAGGGGATCACTATGGTGGGGTGTACCAAAAT 441

Qy        195 TrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProPro 214
              |||:::|||               ||||||   |||||||||:::
Db        442 TGGCAGCAAAATGGTCCTCCACCTCCACCTGATCATGTGCTG----------------- 483

Qy        215 ProLysAlaProSerProProArgGlnProProProProProProProProPheMetSer 234
                 |||   ||||||   |||      ||||||||||||   |||                |||
Db        484 AAGAAGGTGCCTTCGCATCCTTCCCCTCCACCACCTCCTGCTCCACTAAATGTACACAGT 543

Qy        235 SerSerGlyGlySerAspTyrSer------------AspArgProValLeuProProPro 250
                  ||||||:::||||||                 :::|||::::::
Db        544 GGTGGTTCTGGCTCAAATTACTCCGGTGGCGACAACAGCCAACCTCTAGTG--------- 594

Qy        251 SerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArg 270
              |||||||||      ||||||||||||:::   ||||||||||||||:::|||:::
Db        595 TCACCTGGTGCTGCATTGGGTTTTTCAAGGTGTACTTTCACTTATGAGGACTTGTCAGCG 654

Qy        271 AlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHis 290
              ||||||:::||||||||||:::||||||||||||||||||||||||||||||||||||||
Db        655 GCGACCGATGGATTCTCCGATGCTAATCTGCTCGGACAGGGCGGTTTTGGGTATGTTCAC 714

Qy        291 LysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGly 310
              ||||||||||||||:::|||   |||||||||||||||||||:::   |||||||||
Db        715 AAAGGAGTTCTGCCGAATGGGACAGAGGTTGCTGTGAAGCAATTGAGAGATGGGAGTGGG 774

Qy        311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
                                                                  |||:|||
Db        775 CAGGGAGAGCGTGAATTTCAGGCGGAGGTTGAGATTATCAGCCGGGTACATCACAAGCAT 834

Qy        331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
              ||||||:::|||||||||||||||||:::|||   |||||||||||||||||||:::
Db        835 CTTGTAACATTGGTTGGTTATTGCATTTCTGGAGGGAAGAGGTTGCTTGTCTATGAGTAT 894

Qy        351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              ||||||||||||   ||||||||||||||||||||   ||||||||||||||||||||
Db        895 GTTCCAAACAACACATTGGAGCTCCACTTGCATGGGAGAGGCCGACCAACCATGGAATGG 954

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
                  |||||||||:::||||||||||:::||||||||||||:::|||||||||||||||
Db        955 CCTACAAGATTACGCATTGCTTTGGGTGCTGCGAAGGGATTGGCATATCTTCATGAAGAT 1014

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::||||||||||||||||||||||||||:::::||||||||:::|||   :::
Db       1015 TGCCATCCTAAGATCATTCACCGTGACATAAAGTCAGCAAATATTCTTCTTGACGCGAGA 1074

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||||||||||||||||||||||||||||||:::   ||||||   |||||||||
Db       1075 TTTGAGGCAAAGGTGGCAGATTTCGGACTTGCAAAATTGACTTCTGATAATAACACTCAT 1134

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1135 GTTTCAACCAGAGTAATGGGCACATTTGGGTACCTTGCACCAGAGTATGCGTCTTCTGGC 1194

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              :::||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db       1195 CAGCTAACTGAGAAATCAGATGTCTTTTCTTTCGGAGTAATGCTTCTTGAGCTAATAACT 1254

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||||   :::|||          :::||||||||||||||||||||||
Db       1255 GGCCGCCGTCCTGTGAGATCGAACCAATCACAGATGGATGACAGCTTGGTTGATTGGGCA 1314

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
              |||||||||:::   |||||||||:::   |||:::::::::   |||   |||   :::
Db       1315 AGGCCTTTAATGATGCGAGCATCAGATGATGGCAATTATGATGCTTTAGTGGATCCACGG 1374

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
              :::          |||:::      ||||||||||||||:::|||||||||||||||||
Db       1375 CTAGGACAGGAGTACAATGGTAACGAGATGGCGAGGATGATTGCTTGTGCAGCTGCTTGT 1434

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGly 550
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db       1435 GTACGCCATTCTGCACGCCGACGCCCACGGATGAGCCAGGTTGTTCGGGCCTTGGAAGGC 1494

Qy        551 AsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSer 570
              :::||||||||||   |||||||||||||||:::|||||||||   |||
Db       1495 GATGTGTCATTGGATGATCTGAACGAAGGTGTTCGTCCTGGCCATAGCCGATTCTTGGGA 1554

Qy        571 SerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPhe 590
              ||||||      |||   :::||||||:::      ||||||||||:::||||||||||
Db       1555 TCATAC---AACAGCAACGAGTACGACACGGGCCATTACAATGAAGACCTGAAGAAATTC 1611

Qy        591 ArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThr 610
              ||||||||||||   |||:::                        |||   |||   |||
Db       1612 AGGAAGATGGCATTTGGCAGTGGCAATCTA------------GAGAGCAGCCAGCAAACG 1659

Qy        611 SerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg------ 628
                                  |||:::   |||   |||   |||          :::
Db       1660 CAGCCCACCGAGTTCGTCCCGAATCGATCCGTATCAATGGGGGATGCGCGTCAAATACCG 1719

Qy        629 ------GluMetGluMetGlyLysIleLysArgThrGly 639
                    ||||||||||||||   :::|||:::   |||
Db       1720 GAGACGGAGATGGAGATGGGGAGTTTGAAGAAAGATGGC 1758

RESULT 7
ACF36555
ID   ACF36555 standard; DNA; 1515 BP.
XX
AC   ACF36555;
XX
```

```
DT   18-DEC-2003  (first entry)
XX
DE   Z. mays PERK protein encoding genomic DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; maize; gene;
KW   ds.
XX
OS   Zea mays.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21b; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR
CC   Accession No. AY108241)
XX
SQ   Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                4.23e-41      Length:          1515
Score:                    1668.00       Matches:         321
Percent Similarity:       83.87%        Conservative:    43
Best Local Similarity:    73.96%        Mismatches:      59
Query Match:              48.31%        Indels:          12
DB:                       9             Gaps:            4

US-10-086-464-2 (1-647) x ACF36555 (1-1515)

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSer------GlyGly 238
              |||  |||||||||  ||||||||||||      ::::::||||||          |||
Db         26 CCTCCACAGCCGCCAGG-CCACCACCACCAGCGATGCTAAATAGTAGTGCGGGATCTGGT 84

Qy        239 SerAspTyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPhe 258
              |||:::||||||        :::|||||||||||||||||||||   ||||||||||||
Db         85 TCTAATTACTCTGGCGGCGAGATCCTACCTCCACCATCCCCTGGAGCTGTTCTTGGCTTC 144

Qy        259 SerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAla 278
              ||||||||||||||||||||||||||||||   |||||||||:::|||||||||:::|||
Db        145 TCGAAGAGCACATTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCT 204

Qy        279 AsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLys 298
              |||||||||||||||||||||||||||||||||||:::|||:::||||||:::||||||
Db        205 AATCTCCTTGGACAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAA 264

Qy        299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318
              |||:::||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        265 GAGATTGCTGTAAAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCT 324

Qy        319 GluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        325 GAGGTTGAGATTATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGC 384

Qy        339 IleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeu 358
              |||:::|||   ||||||||||||||||||||||||||||||||||   ||||||
Db        385 ATTTCTGGAGGCAAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTC 444

Qy        359 HisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeu 378
              |||||||||   :::|||||||||||||||||||||||||      ||||||||||||:::|||
Db        445 CACTTACATGCGAAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTG 504

Qy        379 GlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArg 398
              |||:::|||||||||||:::|||||||||||||||||||:::||||||||||||||||||
Db        505 GGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGT 564

Qy        399 AspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPhe 418
              |||||||||||||||||||||:::||||||:::||||||||||||||||||||||||||
Db        565 GACATAAAGGCATCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGATTTT 624

Qy        419 GlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThr 438
              ||||||||||||      :::|||   ||||||||||||||||||||||||||||||||||
Db        625 GGACTCGCAAAGTTCACTACTGATAACAACACCCATGTATCGACAAGAGTAATGGGCACC 684

Qy        439 PheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspVal 458
              |||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        685 TTTGGGTATTTGGCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTA 744

Qy        459 PheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsn 478
              ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db        745 TTTTCCTTCGGAGTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACC 804

Qy        479 AsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSer 498
                   |||:::|||||||||||||||||||||||||||||||||||||||||   ||||||
Db        805 CAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTT 864

Qy        499 GluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGlu 518
              |||   |||:::::::::  |||   |||   ::::::        ::::::
Db        865 GAGGATGGTGAATATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAAT 924

Qy        519 GluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArg 538
              ||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db        925 GAGATGGCAAGAATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGG 984

Qy        539 ProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsn 558
              |||||||||||||||:::|||||||||||||||||||||||||||||   |||||||||
Db        985 CCACGTATGAGTCAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAAT 1044

Qy        559 GluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyr 578
              ||||||:::|||||||||   |||       :::   ||||||      |||:::||||||
Db       1045 GAAGGTGTTCGGCCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTAC 1101

Qy        579 AspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGln 598
              ||||||   ||||||||||||||||||||||||||:::|||||||||
Db       1102 GATTCTGGCCAGTACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC 1161

Qy        599 GluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer 618
                        :::   :::||||||   ||||||||:::||||||      ||||||
Db       1162 ------TATACCAGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCT 1215

Qy        619 GlySerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThr 638
              ||||||||||||||      |||:::|||||||||   |||  :::|||:::
Db       1216 GCATCAAGCAGCGAGGGCCACCAGACGCAAGAGATGGAGTCGGGTGCAATGAAGAAAGGT 1275

Qy        639 Gly-----------------GlnGlyTyrSerGlyProSer 646
              |||                 ||||||||||||   |||
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Db       1276 GGCTACAGTGGTGGCTACAGCTCAGGATACAGCGGAGCCTCG 1317

RESULT 8
ACF36556
ID   ACF36556 standard; DNA; 1488 BP.
XX
AC   ACF36556;
XX
DT   18-DEC-2003  (first entry)
XX
DE   G. max PERK partial EST sequence.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; soybean; gene;
KW   ds.
XX
OS   Glycine max.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 21c; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a G. max PERK EST (expressed sequence tag) partial
CC   sequence (TIGR Accession No. TC123698)
XX
SQ   Sequence 1488 BP; 412 A; 291 C; 348 G; 437 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.24e-40      Length:          1488
Score:                  1637.50       Matches:         312
Percent Similarity:     89.67%        Conservative:    44
Best Local Similarity:  78.59%        Mismatches:      36
Query Match:            47.42%        Indels:          5
DB:                     9             Gaps:            3

US-10-086-464-2 (1-647) x ACF36556 (1-1488)

Qy       253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272
Db         3 GGAATTTCATTGGGGTTCTCTAAGAGCACATTCACGTATGAGGAGTTGGCACGCGCAACT 62

Qy       273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
Db        63 GATGGCTTCTCTGATGCCAACCTCCTTGGACAAGGAGGATTTGGATATGTGCACAGAGGA 122

Qy       293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312
Db       123 ATTCTTCCCAACGGCAAGGAGGTGGCAGTGAAGCAATTGAAGGCTGGAAGCGGGCAAGGG 182

Qy       313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
Db       183 GAGCGTGAATTCCAAGCTGAAGTTGAGATAATTAGCCGTGTCCATCACAAGCATCTTGTT 242

Qy       333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
Db       243 TCTTTGGTTGGATACTGCATCACTGGGTCCCAGAGGCTGCTTGTTTATGAATTTGTTCCC 302

Qy       353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372
Db       303 AACAACACATTGGAATTCCATTTGCATGGAAAAGGGAGACCTACCATGGATTGGCCCACA 362

Qy       373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
Db       363 AGACTAAGAATTGCTTTAGGATCTGCTAAGGGACTGGCGTATCTTCATGAAGATTGTCAT 422

Qy       393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
Db       423 CCTAAGATCATCCATCGTGATATCAAAGCTGCCAACATCCTTCTGGATTTTAAGTTTGAA 482

Qy       413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
Db       483 GCAAAGGTTGCAGATTTCGGTCTTGCAAAGTTTTCTTCTGATGTCAATACTCATGTTTCT 542

Qy       433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
Db       543 ACTCGAGTGATGGGGACTTTTGGGTATTTGGCTCCAGAATATGCTTCTAGTGGAAAACTG 602

Qy       453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472
Db       603 ACAGACAAATCAGATGTTTTCTCCTACGGAGTCATGCTCCTCGAGTTAATAACCGGACGA 662

Qy       473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
Db       663 CGGCCCGTCGATAAAAATCAAACTTTCATGGAGGATAGTTTGGTAGACTGGGCTAGGCCT 722

Qy       493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
Db       723 TTGCTCACACGAGCTTTGGAAGAGGATGATTTTGATTCTATTATTGACCCAAGGCTCCAG 782

Qy       513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
Db       783 AATGACTATGATCCTAATGAGATGGCACGAATGGTGGCTTCTGCTGCGGCTTGCATACGT 842

Qy       533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552
Db       843 CATTCGGCAAAGCGTCGACCAAGGATGAGCCAGGTTGTCCGCGCTCTCGAAGGAGATGTC 902

Qy       553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572
Db       903 TCTCTAGCAGATCTGAATGAAGGAATAAGACCTGGACACAGCACTATGTATAGTTCTCAT 962

Qy       573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592
Db       963 ---GAAAGCTCAGATTATGACACTGCACAGTACAAGGAAGACATGAAAAAGTTCAGGAAA 1019

Qy       593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612
Db      1020 ATGGCATTGGGAACTCAGGAGTATGGTGCAAGCAGTGAGTACAGTGCCGCTACAAGTGAG 1079

Qy       613 TyrGlyLeuTyrProSerGlySerSerSerGluGly---------GlnThrThrArgGlu 629
Db      1080 TATGGTTTAAACCCATCAGGCTCAAGTAGTGAAGCACAGAGCCGCCAAACCACAAGGGAA 1139

Qy       630 MetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSer 646
```

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Db       1140 ATGGAAATGAGAAAGATGAAG---AACAATCAAGGTTTCAGTGGAAGTTCT 1187

RESULT 9
AAF77096
ID   AAF77096 standard; DNA; 2520 BP.
XX
AC   AAF77096;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Arabidopsis gene #2.
XX
KW   Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200114563-A1.
XX
PD   01-MAR-2001.
XX
PF   18-AUG-2000; 2000WO-CA000966.
XX
PR   19-AUG-1999;   99US-0149466P.
PR   13-OCT-1999;   99US-0159122P.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
XX
PI   Goring D,  Silva N;
XX
DR   WPI; 2001-244305/25.
XX
PT   New proline-rich, extensin-like receptor kinase nucleic acids and
PT   polypeptides useful for increasing plant wounding or pathogen resistance,
PT   or for producing transgenic plants with increased wounding or pathogen
PT   resistance.
XX
PS   Example; Fig 12; 91pp; English.
XX
CC   The present invention relates to proline-rich extensin-like receptor
CC   kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC   increasing the resistance of plants to wounding and pathogens. These are
CC   also useful for producing transgenic plants with increased wounding and
CC   pathogen resistance compared with a wild type plant, as well as in assays
CC   for identifying and developing compounds to inhibit and/or enhance
CC   polypeptide function directly
XX
SQ   Sequence 2520 BP; 717 A; 553 C; 537 G; 713 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                2.93e-36        Length:          2520
Score:                    1507.00         Matches:         368
Percent Similarity:       53.47%          Conservative:    79
Best Local Similarity:    44.02%          Mismatches:      146
Query Match:              43.64%          Indels:          244
DB:                       4               Gaps:            22

US-10-086-464-2 (1-647) x AAF77096 (1-2520)

Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22
              |||||||||        :::   |||   ||||||||||||||||||:::   :::|||
Db         36 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 95

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42
              |||      |||         |||   |||:::   ||||||      ||||||
Db         96 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 146

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62
                 :::|||||||||||||   |||   |||   |||:::      |||:::
Db        147 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 206

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82
              ||||||      |||:::      ||||||   |||      |||

Db        207 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 263

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102
                    |||:::                |||||||||:::|||      ||||||
Db        264 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 323

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120
              |||         |||||||||      :::   :::   |||      |||      |||
Db        324 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 374

Qy        121 ProSer-----------------SerProSerProProSerPro------SerSerAsp 132
              |||                    |||   :::|||||||||          ||||||
Db        375 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 434

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145
              |||                    :::|||   ::::::||||||:::   :::|||
Db        435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 494

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165
                    |||:::::::::::   ::::::||||||      ||||||||||:::
Db        495 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 554

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAla--- 184
                    |||::::::|||       |||   |||      |||
Db        555 -----------GACTCCTTCTAC------CCTGAACCCATGAAAGGTAAAAACATATAC 596

Qy        185 ----------------------------------------------------GlyGlyPro 187
                                                                   |||
Db        597 ACACTCTTATGTTTCAACAAATAAGAAGCTTAGATTCTTTCATAAAATTTCAGGAAACCA 656

Qy        188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisVal 207
                          :::|||   :::||||||      |||      |||:::
Db        657 ATATCAATACTATGGAAACAACAACAACAACAATGCTTCACAGAATTATCCGAA------ 710

Qy        208 ValThrSerLeuProProProProLysAlaProSerProPro------------------ 221
                 |||   |||              |||   |||
Db        711 ---------TTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGGTTGGGG 761

Qy        222 ArgGln-ProProProProProProProProPheMetSerSerSerGly------GlySe 239
              |||:::    |||   ||||||||||||||||   |||   :::||||||          ||
Db        762 AGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGATTCTTC 821

Qy        239 rAspTyrSer------AspArgProValLeuProProProSerProGlyLeuValLeuGl 257
              |   ||||||      ||||||||||||||||||||||||||||   |||   |||||
Db        822 CATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGCCCTCGG 881

Qy        257 yPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGl 277
              ||||:::|||||||||||||||||:::|||||||||   ||||||   ||||||:::::
Db        882 ATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTTTACGGA 941

Qy        277 uAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGl 297
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 TGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCCTAGCGG 1001

Qy        297 yLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGl 317
              |||||||||||||||||||   ||||||   ||||||||||||||||||||||||||||
Db       1002 GAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGAGTTTCA 1061

Qy        317 nAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTy 337
              ||||||||||:::||||||||||||||||||||||:::||||||||||||||||||||
Db       1062 AGCTGAGGTCGATATCATTAGCCGTGTGCATCATCGGTATCTTGTTTCTTTGGTTGGATA 1121

Qy        337 rCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGl 357
              ||||||||||      :::|||:::|||||||||||||||||||||||      |||||
Db       1122 TTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAACTTTGGA 1181

Qy        357 uLeuHisLeuHisGly------------------------------------------- 362
              |   ||||||||||||
Db       1182 ATATCATCTTCATGGTTAGACCACTTAAAAACTTTGAGTACTAAGTTTATTTTCTCTAAT 1241

Qy        363 ----------------------------------------Glu-GlyArgProThrM 368
                                                       |||   |||   |
Db       1242 CTATATATTCAAGAAAGTTGTAACCTTAATTTGTTGTTGTAGGGAAAAATCTTCCGGTAA 1301
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Qy        368 etGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuH 388
              |||||:::|||||||||||||:::|||||||||||||:::|||||||||||||:::|||||||
Db       1302 TGGAGTTCTCCACTAGGTTGCGTATCGCCTTAGGTGCTGCGAAAGGACTCGCTTACCTTC 1361

Qy        388 isGluAspCys---------------------------------------------------- 391
              ||||||||||
Db       1362 ACGAAGACTGTAAGTTTTAACATTCACCATTCTCATTTTCTTAACCAAGTTGCATAAAAC 1421

Qy        392 ------------------------------------------------------------Asn 392
                                                                          :::
Db       1422 AGAGAAAGCTCTGTCTCTGACTAGTGTTATCTTTTTGGCTGAGAAAATGGTGCAGGCCAT 1481

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
              |||:::||||||||||||||||||||||:::::|||||||||:::||||||   |||:::
Db       1482 CCTCGGATCATTCACCGCGACATCAAGTCTGCAAATATTCTCTTGGACTTCAACTTTGAT 1541

Qy        413 Ala------------------------------------------------------------ 413
              |||
Db       1542 GCTATGGTGATAAACTAGTAGCTTGCATTCATCTACGGTTTTTTGTTAAGACTACATTGA 1601

Qy        414 ----------------------LysValAlaAspPheGlyLeuAlaLysIleAlaSerAs 426
                                   :::|||||||||||||||||||||||:::   |||||
Db       1602 TGACATTTTGCATTTGTTTATTCAGGTGGCTGATTTTGGATTAGCTAAGTTAACATCTGA 1661

Qy        426 pThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly---------------- 440
              |   |||||||||||||||||||||||||||||||||||||| |||
Db       1662 TAACAACACTCATGTATCTACTCGTGTGATGGGAACTTTCGGGTAAGCGTTTTACCGTAT 1721

Qy        440 ------------------------------------------------------------ 440

Db       1722 GATAAGATTGTTCGTGACACTCAAGAAACATAACCTTTGTAGACTAATCTACTTTGCTTC 1781

Qy        441 --------------------TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrG 454
                                 |||||||||||||||||||:::|||||||||||||||||
Db       1782 TTTCCACAAACATGTGTAGATATCTAGCTCCAGAATATGCTTCAAGCGGTAAATTAACCG 1841

Qy        454 luLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgP 474
              ||||||||||||||||||||:::|||||||:::|||||||||||||||||||||:::||||
Db       1842 AGAAATCCGATGTTTTCTCTTACGGAGTTATGTTATTGGAACTTATAACTGGAAAACGAC 1901

Qy        474 roValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp------------- 489
              ||||||||   |||::::::   :::||||||:::||||||||||||
Db       1902 CGGTTGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGTATTCATGCATG 1958

Qy        489 ------------------------------------------------------------ 489

Db       1959 TAACATATGTATCGTGTATATATGTTTTTCGCCTTTTTCGCGTACTAATGATCATGAATA 2018

Qy        490 ---AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
                 ||||||||||||:::   ||||||   |||   |||:::|||       |||||||||
Db       2019 CAGGCTCGGCCTCTTATGGCTCGCGCGCTAGAAGATGGAAACTTTAATGAGCTCGCAGAT 2078

Qy        509 AlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528
              |||::::::         |||:::   :::||||||||||||||||   |||||||||
Db       2079 GCGAGGCTTGAAGGCAACTACAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCCGCT 2138

Qy        529 AlaCysValArgHisSerAlaArgArgArgProArgMetSer----------------- 542
              |||   :::|||||||||   |||:::||||||:::|||
Db       2139 GCTAGCATTCGTCATTCGGGGCGTAAACGTCCAAAGATGAG-CCAGGTGAATCAAAATTA 2197

Qy        543 ------------------------------------------------GlnIleVal 545
                                                              ||||||||
Db       2198 TAACTAAAAGTCTATTTTTGTCAGAGAATAACAAACAAATGTTGTGGTTTTCAGATAGTA 2257

Qy        546 ArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGln 565
              ||||||||||||||   |||||||||      ||||||||||||:::::||||||
Db       2258 AGAGCGTTAGAAGGAGAAGTGTCCTTAGATGCTTTAAACGAAGGTGTGAAGCCAGGACAC 2317

Qy        566 SerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGlu 585
              ||||||||||||   |||   |||   |||:::||||||      :::   ||||||
Db       2318 AGTAACGTTTACGGGTCATTGGGAGCAAGCTCGGATTATAGTCAGACATCTTACAATGCA 2377

Qy        586 AspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr---------AsnAla 602
              ||||||||||||||||||:::::||||||   :::||||||:::         :::
Db       2378 GACATGAAGAAATTCAGACAGATAGCTTTGTCGAGCCAAGAATTCCCAGTCAGTGACTGT 2437

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
                 |||      ||||||   :::   |||   |||
Db       2438 GAAGGAACATCTAGTAATGATTCTAGAGATATGGGA 2473
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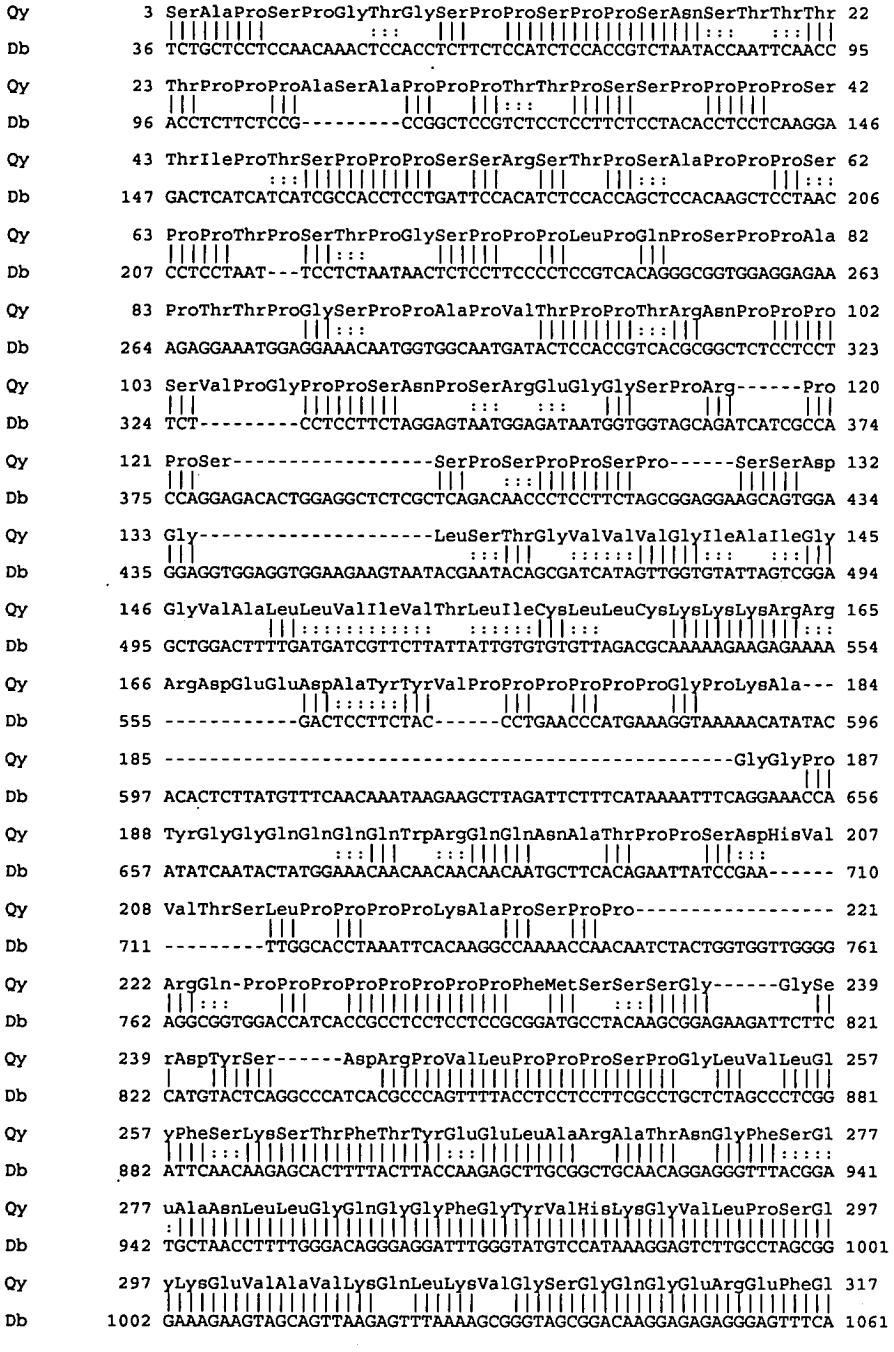
RESULT 10
ACF36551
ID ACF36551 standard; DNA; 2520 BP.
XX
AC ACF36551;
XX
DT 18-DEC-2003 (first entry)
XX
DE Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
DR P-PSDB; ABR82940.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 12; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents a PERK1 polypeptide related protein encoding genomic
CC DNA from A. thaliana (Accession NO. AAD15491)
XX
SQ Sequence 2520 BP; 717 A; 552 C; 538 G; 713 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.58e-36	Length:	2520
Score:	1504.00	Matches:	367
Percent Similarity:	53.47%	Conservative:	80
Best Local Similarity:	43.90%	Mismatches:	146
Query Match:	43.56%	Indels:	244
DB:	9	Gaps:	22

US-10-086-464-2 (1-647) x ACF36551 (1-2520)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Db 36 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 95
Qy 23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42
Db 96 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 146
Qy 43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62
Db 147 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 206
Qy 63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82
Db 207 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 263
Qy 83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102
Db 264 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 323
Qy 103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120
Db 324 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 374
Qy 121 ProSer-----------------SerProSerProProSerPro------SerSerAsp 132
Db 375 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 434
Qy 133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145
Db 435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 494
Qy 146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165
Db 495 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTGTTAGACGCAAAAAGAAGAGAAAA 554
Qy 166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAla--- 184
Db 555 ------------GACTCCTTCTAC------CCTGAACCCATGAAAGGTAAAAACATATAC 596
Qy 185 --GlyGlyPro 187
Db 597 ACACTCTTATGTTTCAACAAATAAGAAGCTTAGATTCTTTCATAAAATTTCAGGAAACCA 656
Qy 188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisVal 207
Db 657 ATATCAATACTATGGAAACAACAACAACAACAATGCTTCACAGAATTATCCGAA------ 710
Qy 208 ValThrSerLeuProProProProLysAlaProSerProPro----------------- 221
Db 711 ---------TTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGGTTGGGG 761
Qy 222 ArgGln-ProProProProProProProProPheMetSerSerSerGly------GlySe 239
Db 762 AGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGATTCTTC 821
Qy 239 rAspTyrSer------AspArgProValLeuProProProSerProGlyLeuValLeuGl 257
Db 822 CATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGCCCTCGG 881
Qy 257 yPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGl 277
Db 882 ATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTTTACGGA 941
Qy 277 uAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGl 297
Db 942 TGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCCTAGCGG 1001
Qy 297 yLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGl 317
Db 1002 GAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGAGTTTCA 1061
Qy 317 nAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTy 337
Db 1062 AGCTGAGGTCGATATCATTAGCCGTGTGCATCATCGGTATCTTGTTTCTTTGGTTGGATA 1121
Qy 337 rCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGl 357
Db 1122 TTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAACTTTGGA 1181
Qy 357 uLeuHisLeuHisGly-- 362
Db 1182 ATATCATCTTCATGGTTAGACCACTTAAAAACTTTGAGTACTAAGTTTATTTTCTCTAAT 1241
Qy 363 --Glu-GlyArgProThrM 368
Db 1242 CTATATATTCAAGAAAGTTGTAACCTTAATTTGTTGTTGTAGGGAAAAATCTTCCGGTAA 1301
Qy 368 etGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuH 388
Db 1302 TGGAGTTCTCCACTAGGTTGCGTATCGCCTTAGGTGCTGCGAAAGGACTCGCTTACCTTC 1361
Qy 388 isGluAspCys-- 391
Db 1362 ACGAAGACTGTAAGTTTTAACATTCACCATTCTCATTTTCTTAACCAAGTTGCATAAAAC 1421
Qy 392 --Asn 392
Db 1422 AGAGAAAGCTCTGTCTCTGACTAGTGTTATCTTTTTGGCTGAGAAAATGGTGCAGGCCAT 1481
Qy 393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
Db 1482 CCTCGGATCATTCACCGCGACATCAAGTCTGCAAATATTCTCTTGGACTTCAACTTTGAT 1541
Qy 413 Ala-- 413
Db 1542 GCTATGGTGATAAACTAGTAGCTTGCATTCATCTACGGTTTTTTGTTAAGACTACATTGA 1601
Qy 414 ----------------------LysValAlaAspPheGlyLeuAlaLysIleAlaSerAs 426
Db 1602 TGACATTTTGCATTTGTTTATTCAGGTGGCTGATTTTGGATTAGCTAAGTTAACATCTGA 1661
Qy 426 pThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly---------------- 440
Db 1662 TAACAACACTCATGTATCTACTCGTGTGATGGGAACTTTCGGGTAAGCGTTTTACCGTAT 1721
Qy 440 -- 440
Db 1722 GATAAGATTGTTCGTGACACTCAAGAAACATAACCTTTGTAGACTAATCTACTTTGCTTC 1781
Qy 441 --------------------TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrG 454
Db 1782 TTTCCACAAACATGTGTAGATATCTAGCTCCAGAATATGCTTCAAGCGGTAAATTAACCG 1841
Qy 454 luLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgP 474
Db 1842 AGAAATCCGATGTTTTCTCTTACGGAGTTATGTTATTGGAACTTATAACTGGAAAACGAC 1901
Qy 474 roValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp------------- 489
Db 1902 CGGTTGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGTATTCATGCATG 1958
Qy 489 -- 489
Db 1959 TAACATATGTATCGTGTATATATGTTTTTCGCCTTTTTCGCGTACTAATGATCATGAATA 2018
Qy 490 ---AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
Db 2019 CAGGCTCGGCCTCTTATGGCTCGCGCGCTAGAAGATGGAAACTTTAATGAGCTCGCAGAT 2078
Qy 509 AlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528
Db 2079 GCGAGGCTTGAAGGCAACTACAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCCGCT 2138
Qy 529 AlaCysValArgHisSerAlaArgArgArgProArgMetSer----------------- 542

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Db       2139 GCTAGCATTCGTCATTCGGGGCGTAAACGTCCAAAGATGAG-CCAGGTGAATCAAAATTA 2197

Qy        543 ----------------------------------------------------GlnIleVal 545

Db       2198 TAACTAAAAGTCTATTTTTGTCAGAGAATAACAAACAAATGTTGTGGTTTTCAGATAGTA 2257

Qy        546 ArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGln 565

Db       2258 AGAGCGTTAGAAGGAGAAGTGTCCTTAGATGCTTTAAACGAAGGTGTGAAGCCAGGACAC 2317

Qy        566 SerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGlu 585

Db       2318 AGTAACGTTTACGGGTCATTGGGAGCAAGCTCGGATTATAGTCAGACATCTTACAATGCA 2377

Qy        586 AspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr---------AsnAla 602

Db       2378 GACATGAAGAAATTCAGACAGATAGCTTTGTCGAGCCAAGAATTCCCAGTCAGTGACTGT 2437

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGly 614

Db       2438 GAAGGAACATCTAGTAATGATTCTAGAGATATGGGA 2473
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RESULT 11
AAF77097
ID AAF77097 standard; DNA; 2820 BP.
XX
AC AAF77097;
XX
DT 17-MAY-2001 (first entry)
XX
DE Arabidopsis gene #3.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,
PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Example; Fig 13; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 2820 BP; 819 A; 629 C; 577 G; 795 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2e-35 Length: 2820
Score: 1479.50 Matches: 367

Percent Similarity: 50.00% Conservative: 99
Best Local Similarity: 39.38% Mismatches: 151
Query Match: 42.85% Indels: 318
DB: 4 Gaps: 28

US-10-086-464-2 (1-647) x AAF77097 (1-2820)

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Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20

Db         52 GTGGATTCATCTCCTGCCCCTGAAACC---TCAAATGGGACACCACCGTCAAACGGAACA 108

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40

Db        109 TCG---------CCGTCTAATGAGTCATCGCCGCCAACACCACCTTCTTCACCACCACCA 159

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60

Db        160 TCATCA---------ATATCTGCTCCTCCGCCAGATATCTCCGCTTCTTTTTCACCGCCG 210

Qy         61 ProSerProProThr---------------ProSerThrProGlySerProProProLeu 75

Db        211 CCTGCACCACCAACGCAAGAAACGTCACCTCCTACATCTCCGTCCTCATCGCCGCCTGTT 270

Qy         76 ---------------ProGln------------ProSerProProAlaPro------Thr 84

Db        271 GTAGCTAATCCGTCACCGCAGACTCCAGAGAATCCTTCTCCACCTGCACCTGAAGGCTCA 330

Qy         85 ThrProGlySerProProAla---ProValThrPro------------ProThrArgAsn 99

Db        331 ACTCCTGTAACGCCACCTGCACCACCACAAACACCGTCGAACCAATCACCGGAAAGACCA 390

Qy        100 ProProPro---------------------------------------------------- 102

Db        391 ACTCCTCCTTCTCCTGGTGCCAATGATGACCGAAACAGAACCAATGGCGGAAACAACAAC 450

Qy        103 ---------SerValProGlyProProSerAsnProSerArg---------GluGlyGly 116

Db        451 AGAGACGGCTCCACACCATCACCACCGTCGTCAGGGAACAGAACTTCCGGTGACGGTGGC 510

Qy        117 SerProArgProProSerSerProSerProProSerProSerSerAspGlyLeuSerThr 136

Db        511 TCACCTTCACCACCTCGGTCGATAAGCCCTCCTCAGAATAGTGGAGATTCAGACTCATCA 570

Qy        137 --------------------------GlyValValValGlyIleAlaIleGlyGlyVal 147

Db        571 TCGGGTAATCATCCACAAGCCAACATTGGATTGATTATTGGAGTCCTTGTAGGAGCAGGG 630

Qy        148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAsp 167

Db        631 CTTTTGCTTCTACTTGCAGTGTGTATTTGCATCTGTTGCAACAGGAAGAAGAAGAAGAAA 690

Qy        168 GluGluAspAla---------TyrTyrValProProProProProProGlyProLysAla 184

Db        691 TCTCCTCAGGTCAACCACATGCACTACTACAATAACAATCCTTATGGAGGAGCACCCTCA 750

Qy        185 Gly---------------------------------------------------------- 185

Db        751 GGTAATTACAGTTTAGTATAACTGGAATTTAATTTGTAGCCTAATGGTGTTTGATTAGGT 810

Qy        186 --------------------------------GlyProTyrGlyGlyGlnGlnGlnGln 194

Db        811 TTCAGAACGATCATAGTCTAATGGTTTCTGCTAGCTCCATATGGCAAAAGGATTAGATT- 869

Qy        195 TrpArgGlnGlnAsnAlaThr---------------------------------ProPro 203

Db        870 TATAAGCTAAAGGAGATGTTGCATAGTGTAGGTAATGGTGGTTATTACAAGGGAACACCT 929

Qy        204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223

Db        930 CAAGATCATGTGGTG---AATATGGCTGGTCAAGGAGGTGGGAATTGGGGTCCACAGCAA 986

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
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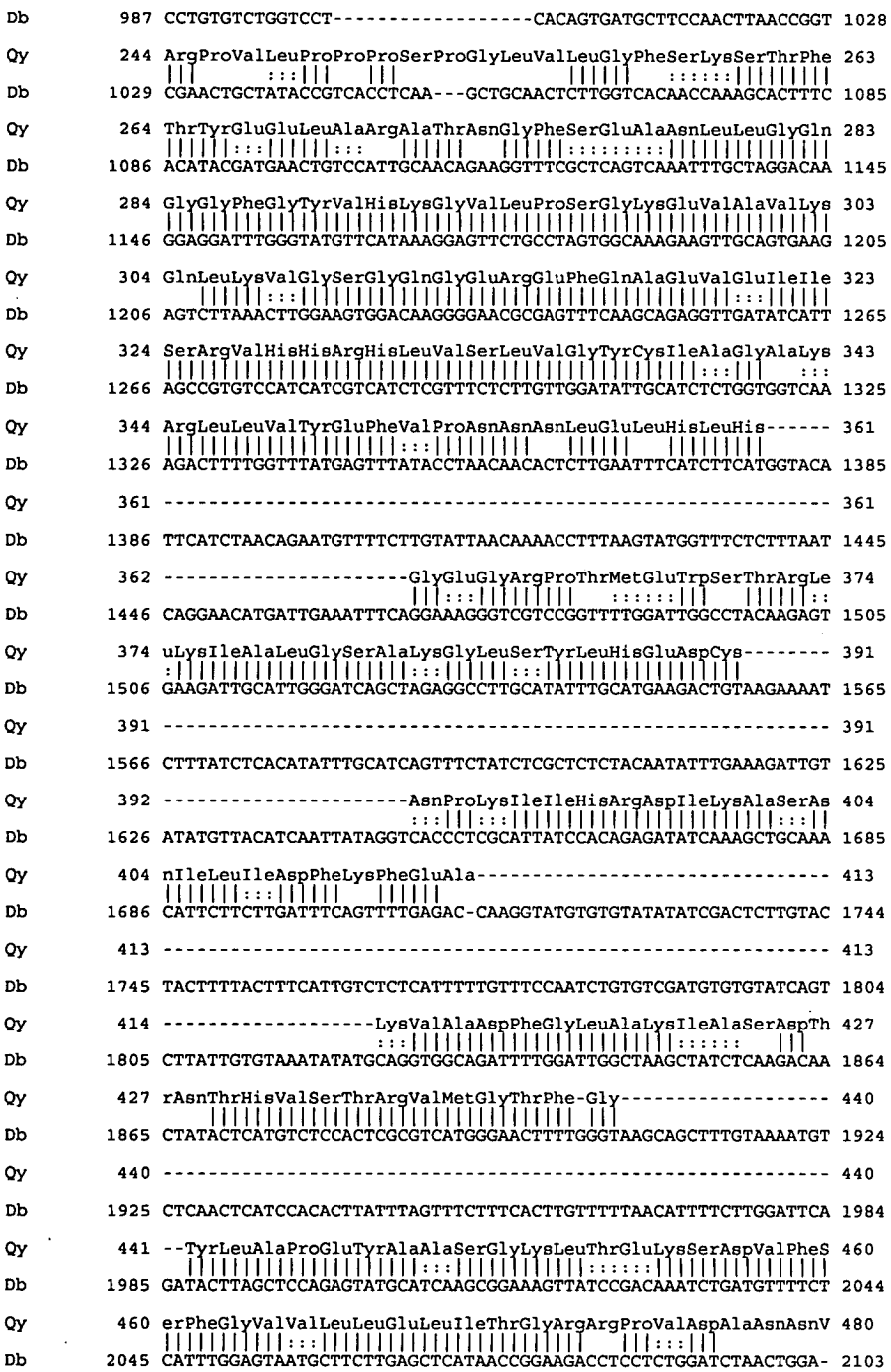

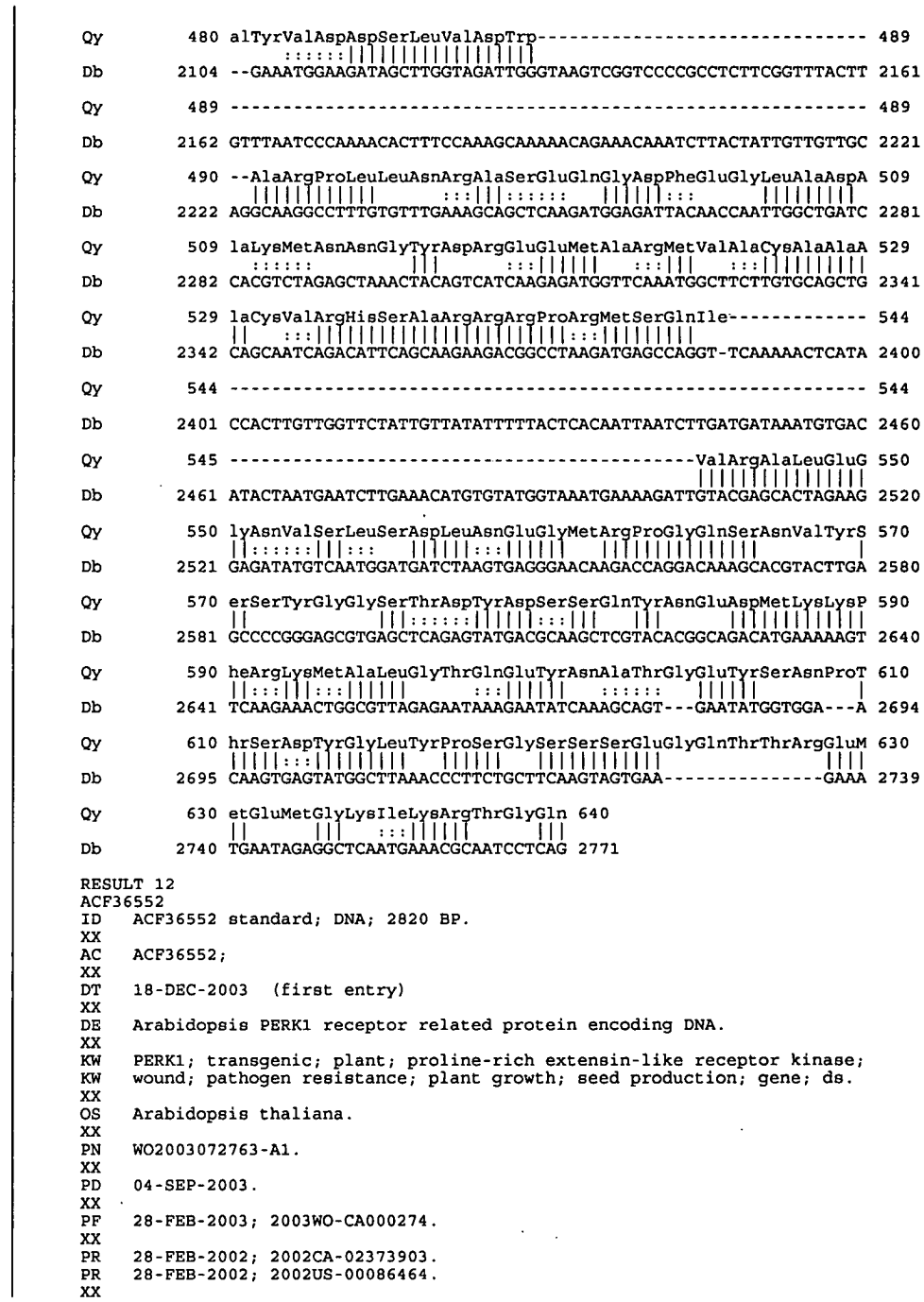

RESULT 12
ACF36552
ID ACF36552 standard; DNA; 2820 BP.
XX
AC ACF36552;
XX
DT 18-DEC-2003 (first entry)
XX
DE Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX

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PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82941.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 13; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a PERK1 polypeptide related protein encoding genomic
CC   DNA from A. thaliana (Accession NO. CAA18823)
XX
SQ   Sequence 2820 BP; 819 A; 630 C; 576 G; 795 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                3.42e-35       Length:          2820
Score:                    1471.50        Matches:         366
Percent Similarity:       49.89%         Conservative:    99
Best Local Similarity:    39.27%         Mismatches:      152
Query Match:              42.62%         Indels:          318
DB:                       9              Gaps:            28

US-10-086-464-2 (1-647) x ACF36552 (1-2820)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
              :::   |||:::|||:::|||   |||   |||       :::||||||||||||   |||
Db         52 GTGGATTCATCTCCTGCCCCTGAAACC---TCAAATGGGACACCACCGTCAAACGGAACA 108

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
              :::         |||         :::   |||||||||   ||||||||||||||||||
Db        109 TCG---------CCGTCTAATGAGTCATCGCCGCCAACACCACCTTCTTCACCACCACCA 159

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
                 |||             |||   ||||||          |||          :::||||||
Db        160 TCATCA---------ATATCTGCTCCTCCGCCAGATATCTCCGCTTCTTTTTCACCGCCG 210

Qy         61 ProSerProProThr---------------ProSerThrProGlySerProProProLeu 75
              |||:::|||||||||                |||:::::::|||   |||   ||||||:::
Db        211 CCTGCACCACCAACGCAAGAAACGTCACCTCCTACATCTCCGTCCTCATCGCCGCCTGTT 270

Qy         76 ---------------ProGln------------ProSerProProAlaPro------Thr 84
                           ||||||                ||||||||||||||||||      :::
Db        271 GTAGCTAATCCGTCACCGCAGACTCCAGAGAATCCTTCTCCACCTGCACCTGAAGGCTCA 330

Qy         85 ThrProGlySerProProAla---ProValThrPro------------ProThrArgAsn 99
              ||||||   :::|||||||||   |||   ||||||             |||   |||
Db        331 ACTCCTGTAACGCCACCTGCACCACCACAAACACCGTCGAACCAATCACCGGAAAGACCA 390

Qy        100 ProProPro------------------------------------------------- 102
              ||||||
Db        391 ACTCCTCCTTCTCCTGGTGCCAATGATGACCGAAACAGAACCAATGGCGGAAACAACAAC 450

Qy        103 ---------SerValProGlyProProSerAsnProSerArg---------GluGlyGly 116
                     |||   |||   |||||||||:::   :::|||         :::|||||||
Db        451 AGAGACGGCTCCACACCATCACCACCGTCGTCAGGGAACAGAACTTCCGGTGACGGTGGC 510

Qy        117 SerProArgProProSerSerProSerProProSerProSerSerAspGlyLeuSerThr 136
              ||||||   ||||||   |||   |||||||||       |||   |||       |||:::
Db        511 TCACCTTCACCACCTCGGTCGATAAGCCCTCCTCAGAATAGTGGAGATTCAGACTCATCA 570

Qy        137 --------------------------GlyValValValGlyIleAlaIleGlyGlyVal 147
                                        |||:::::::::|||:::   :::|||
Db        571 TCGGGTAATCATCCACAAGCCAACATTGGATTGATTATTGGAGTCCTTGTAGGAGCAGGG 630

Qy        148 AlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAsp 167
                 ||||||::::::          ||||||:::   |||   :::|||:::::::::
Db        631 CTTTTGCTTCTACTTGCAGTGTGTATTTGCATCTGTTGCAACAGGAAGAAGAAGAAGAAA 690

Qy        168 GluGluAspAla---------TyrTyrValProProProProProProGlyProLysAla 184
                             :::|||                |||       |||       :::
Db        691 TCTCCTCAGGTCAACCACATGCACTACTACAATAACAATCCTTATGGAGGAGCACCCTCA 750

Qy        185 Gly------------------------------------------------------- 185
              |||
Db        751 GGTAATTACAGTTTAGTATAACTGGAATTTAATTTGTAGCCTAATGGTGTTTGATTAGGT 810

Qy        186 --------------------------------GlyProTyrGlyGlyGlnGlnGlnGln 194
                                             |||||||||   :::   :::
Db        811 TTCAGAACGATCATAGTCTAATGGTTTCTGCTAGCTCCATATGGCAAAAGGATTAGATT- 869

Qy        195 TrpArgGlnGlnAsnAlaThr---------------------------------ProPro 203
              ::::::   :::                                          |||
Db        870 TATAAGCTAAAGGAGATGTTGCATAGTGTAGGTAATGGTGGTTATTACAAGGGAACACCT 929

Qy        204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223
                 ||||||||||||   ::::::                                |||:::|||
Db        930 CAAGATCATGTGGTG---AATATGGCTGGTCAAGGAGGTGGGAATTGGGGTCCACAGCAA 986

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
              |||          |||                   |||     |||:::   :::
Db        987 CCTGTGTCTGGTCCT-----------------CACAGTGATGCTTCCAACTTAACCGGT 1028

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
              |||       :::|||   |||                 ||||||   ::::::|||||||||
Db       1029 CGAACTGCTATACCGTCACCTCAA---GCTGCAACTCTTGGTCACAACCAAAGCACTTTC 1085

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
              ||||||:::||||||:::   ||||||   ||||||::::::::::|||||||||||||||
Db       1086 ACATACGATGAACTGTCCATTGCAACAGAAGGTTTCGCTCAGTCAAATTTGCTAGGACAA 1145

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 GGAGGATTTGGGTATGTTCATAAAGGAGTTCTGCCTAGTGGCAAAGAAGTTGCAGTGAAG 1205

Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
              ||||||:::||||||||||||||||||||||||||||||||||||||||:::||||||
Db       1206 AGTCTTAAACTTGGAAGTGGACAAGGGGAACGCGAGTTTCAAGCAGAGGTTGATATCATT 1265

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::      :::
Db       1266 AGCCGTGTCCATCATCGTCATCTCGTTTCTCTTGTTGGATATTGCATCTCTCGTGGTCAA 1325

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis------ 361
              ||||||||||||||||||:::|||||||||   ||||||   |||||||||
Db       1326 AGACTTTTGGTTTATGAGTTTATACCTAACAACACTCTTGAATTTCATCTTCATGGTACA 1385

Qy        361 ------------------------------------------------------------ 361

Db       1386 TTCATCTAACAGAATGTTTTCTTGTATTAACAAAACCTTTAAGTATGGTTTCTCTTTAAT 1445

Qy        362 ----------------------GlyGluGlyArgProThrMetGluTrpSerThrArgLe 374
                                     |||:::|||||||||   ::::::|||   ||||||::
Db       1446 CAGGAACATGATTGAAATTTCAGGAAAGGGTCGTCCGGTTTTGGATTGGCCTACAAGAGT 1505

Qy        374 uLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys-------- 391
              :|||||||||||||||||||:::|||||||:::|||||||||||||||||||
Db       1506 GAAGATTGCATTGGGATCAGCTAGAGGCCTTGCATATTTGCATGAAGACTGTAAGAAAAT 1565
```

```
Qy        391 ------------------------------------------------------------ 391

Db       1566 CTTTATCTCACATATTTGCATCAGTTTCTATCTCGCTCTCTACAATATTTGAAAGATTGT 1625

Qy        392 ---------------------AsnProLysIleIleHisArgAspIleLysAlaSerAs 404
                                  :::|||:::|||||||||||||||||||||||||:::||
Db       1626 ATATGTTACATCAATTATAGGTCACCCTCGCATTATCCACAGAGATATCAAAGCTGCAAA 1685

Qy        404 nIleLeuIleAspPheLysPheGluAla------------------------------- 413
               |||||||:::||||||   ||||||
Db       1686 CATTCTTCTTGATTTCAGTTTTGAGAC-CAAGGTATGTGTGTATATATCGACTCTTGTAC 1744

Qy        413 ------------------------------------------------------------ 413

Db       1745 TACTTTTACTTTCATTGTCTCTCATTTTTGTTTCCAATCTGTGTCGATGTGTGTATCAGT 1804

Qy        414 ------------------LysValAlaAspPheGlyLeuAlaLysIleAlaSerAspTh 427
                              :::||||||||||||||||||||||||:::::::   |||
Db       1805 CTTATTGTGTAAATATATGCAGGTGGCAGATTTTGGATTGGCTAAGCTATCTCAAGACAA 1864

Qy        427 rAsnThrHisValSerThrArgValMetGlyThrPhe-Gly------------------- 440
               |||||||||||||||||||||||||||||||||| |||
Db       1865 CTATACTCATGTCTCCACTCGCGTCATGGGAACTTTTGGGTAAGCAGCTTTGTAAAATGT 1924

Qy        440 ------------------------------------------------------------ 440

Db       1925 CTCAACTCATCCACACTTATTTAGTTTCTTTCACTTGTTTTTAACATTTTCTTGGATTCA 1984

Qy        441 --TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheS 460
                 |||||||||||||||||||:::|||||||||||:::::::|||||||||||||||||
Db       1985 GATACTTAGCTCCAGAGTATGCATCAAGCGGAAAGTTATCCGACAAATCTGATGTTTTCT 2044

Qy        460 erPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnV 480
               ||||||||||:::|||||||||||||||||||||||||   |||:::|||
Db       2045 CATTTGGAGTAATGCTTCTTGAGCTCATAACCGGAAGACCTCCTCTGGATCTAACTGGA- 2103

Qy        480 alTyrValAspAspSerLeuValAspTrp------------------------------ 489
                    ::::::|||||||||||||||||||
Db       2104 --GAAATGGAAGATAGCTTGGTAGATTGGGTAAGTCGGTCCCCGCCTCTTCGGTTTACTT 2161

Qy        489 ------------------------------------------------------------ 489

Db       2162 GTTTAATCCCAAAACACTTTCCAAAGCAAAAACAGAAACAAATCTTACTATTGTTGTTGC 2221

Qy        490 --AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspA 509
                 ||||||||||||      :::|||::::::   ||||||:::      |||||||||
Db       2222 AGGCAAGGCCTTTGTGTTTGAAAGCAGCTCAAGATGGAGATTACAACCAATTGGCTGATC 2281

Qy        509 laLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaA 529
                 ::::::          |||      :::||||||   :::|||   :::||||||||||
Db       2282 CACGTCTAGAGCTAAACTACAGTCATCAAGAGATGGTTCAAATGGCTTCTTGTGCAGCTG 2341

Qy        529 laCysValArgHisSerAlaArgArgArgProArgMetSerGlnIle------------- 544
               ||   :::|||||||||||||||||||||||:::|||||||||
Db       2342 CAGCAATCAGACATTCAGCAAGAAGACGGCCTAAGATGAGCCAGGT-TCAAAAACTCATA 2400

Qy        544 ------------------------------------------------------------ 544

Db       2401 CCACTTGTTGGTTCTATTGTTATATTTTTACTCACAATTAATCTTGATGATAAATGTGAC 2460

Qy        545 ---------------------------------------------ValArgAlaLeuGluG 550
                                                           |||||||||||||||
Db       2461 ATACTAATGAATCTTGAAACATGTGTATGGTAAATGAAAAGATTGTACGAGCACTAGAAG 2520

Qy        550 lyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrS 570
               ||::::::|||:::   |||||||:::||||||   ||||||||||||||         |
Db       2521 GAGATATGTCAATGGATGATCTAAGTGAGGGAACAAGACCAGGACAAAGCACGTACTTGA 2580

Qy        570 erSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysP 590
               ||           |||::::::|||||:::|||   |||      ||||||||||||
Db       2581 GCCCCGGGAGCGTGAGCTCAGAGTATGACGCAAGCTCGTACACGGCAGACATGAAAAAGT 2640

Qy        590 heArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProT 610
                  ||:::|||:::||||||      :::||||||   ::::::   ||||||         |
Db       2641 TCAAGAAACTGGCGTTAGAGAATAAAGAATATCAAAGCAGT---GAATATGGTGGA---A 2694

Qy        610 hrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluM 630
               |||||:::|||||||||   ||||||   ||||||||||||               ||||
Db       2695 CAAGTGAGTATGGCTTAAACCCTTCTGCTTCAAGTAGTGAA--------------GAAA 2739

Qy        630 etGluMetGlyLysIleLysArgThrGlyGln 640
               ||      |||   :::||||||      |||
Db       2740 TGAATAGAGGCTCAATGAAACGCAATCCTCAG 2771
```

RESULT 13
AAF77095
ID AAF77095 standard; DNA; 2880 BP.
XX
AC AAF77095;
XX
DT 17-MAY-2001 (first entry)
XX
DE Arabidopsis gene #1.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,
PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Example; Fig 11; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 2880 BP; 814 A; 693 C; 569 G; 804 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.5e-27	Length:	2880
Score:	1209.50	Matches:	325
Percent Similarity:	43.85%	Conservative:	92
Best Local Similarity:	34.17%	Mismatches:	160
Query Match:	35.03%	Indels:	376
DB:	4	Gaps:	26

US-10-086-464-2 (1-647) x AAF77095 (1-2880)

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Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThr 21
                :::||||||      |||         |||||||||||||||||:::::|||::::::
Db         98 AACTCAGCTCTTCCACCTGTTGATTCCTCTCCTCCTAGTCCACCAGCTGATTCATCATCA 157

Qy         22 Thr--------------------ThrProProProAlaSer----------------- 28
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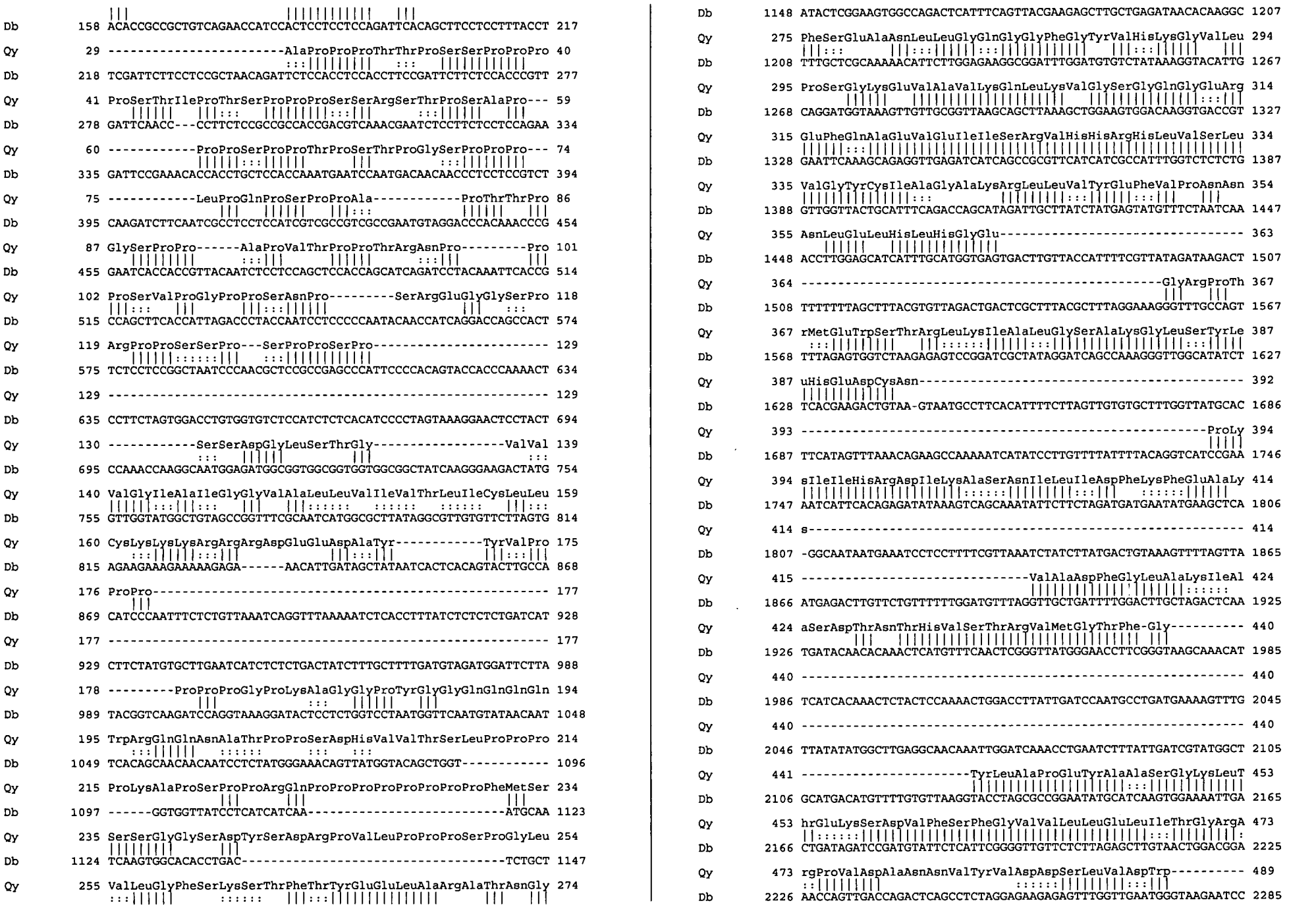

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Qy        489 ------------------------------------------------------------ 489

Db       2286 AACTTTCAAACATTCTTCAATAATAGTAAGATTGGCCCTAGTATACTTATATAGTACTTA 2345

Qy        490 --------------AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGlu 504
                           ||||||||||||||   :::|||   |||   ||||||
Db       2346 TAAATGAACTCACAGGCGCGCCCGCTGCTTCTCAAAGCCATTGAGACCGGAGATTTAAGC 2405

Qy        505 GlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVal 524
              |||   |||   ::::::          |||          |||:::   ||||||:::
Db       2406 GAACTGATTGATACACGGCTTGAAAAGCGTTATGTGGAGCATGAAGTCTTCAGAATGATC 2465

Qy        525 AlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln--- 543
                 ||||||||||||||||||||||||||      :::||||||||||||   |||
Db       2466 GAGACAGCCGCTGCATGTGTTAGACATTCTGGTCCAAAACGCCCACGCATGGTTCAGGTA 2525

Qy        543 ------------------------------------------------------------ 543

Db       2526 ATTCTGACTAACCAAAAGTCCAAAGCTCCCATATATAGTAACAAGTGATTTCTCACATCT 2585

Qy        544 --------------------------IleValArgAlaLeuGluGlyAsnValSerLeu 554
                                       :::||||||||||||:::   :::
Db       2586 GAAAACTTATCTACTCTTCGAAATAAGGTTGTGAGAGCATTGGACTGCGACGGAGACTCG 2645

Qy        555 SerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGly 574
              |||::::::   |||::::::   ||||||
Db       2646 GGAGATATTAGCAACGGAATCAAAATTGGGCAA-------------------------- 2678

Qy        575 SerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAla 594
              ||||||   |||||||||   ||||||||||||||:::   ||||||||||||||||||
Db       2679 AGCACAACTTATGACTCAGGGCAATACAATGAAGACATTATGAAATTCAGGAAAATGGCG 2738

Qy        595 LeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGly 614
              |||          :::|||   ||||||                    |||
Db       2739 TTTGGTGGTGATAACAGCGTAGAGTCAGGATTGTACAGT----------------GGA 2780

Qy        615 LeuTyrProSerGlySerSerSerGlu 623
              |||   :::   |||||||||:::
Db       2781 AACTACTCTGCCAAAAGCTCTTCAGAT 2807

RESULT 14
ACF36550
ID   ACF36550 standard; DNA; 2880 BP.
XX
AC   ACF36550;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82939.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 11; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a PERK1 polypeptide related protein encoding genomic
CC   DNA from A. thaliana (Accession NO. AAC98010)
XX
SQ   Sequence 2880 BP; 814 A; 693 C; 569 G; 804 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-27       Length:          2880
Score:                  1209.50       Matches:         325
Percent Similarity:     43.85%        Conservative:    92
Best Local Similarity:  34.17%        Mismatches:      160
Query Match:            35.03%        Indels:          376
DB:                     9             Gaps:            26

US-10-086-464-2 (1-647) x ACF36550 (1-2880)

Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThr 21
              :::||||||      |||         ||||||||||||||||||:::::|||:::::::
Db         98 AACTCAGCTCTTCCACCTGTTGATTCCTCTCCTCCTAGTCCACCAGCTGATTCATCATCA 157

Qy         22 Thr---------------------ThrProProProAlaSer------------------ 28
              |||                    ||||||||||||   |||
Db        158 ACACCGCCGCTGTCAGAACCATCCACTCCTCCTCCAGATTCACAGCTTCCTCCTTTACCT 217

Qy         29 ------------------------AlaProProProThrThrProSerSerProProPro 40
                                      :::|||||||||   :::   ||||||||||||
Db        218 TCGATTCTTCCTCCGCTAACAGATTCTCCACCTCCACCTTCCGATTCTTCTCCACCCGTT 277

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaPro--- 59
                ||||||   |||:::   |||||||||:::|||      :::||||||   |||
Db        278 GATTCAACC---CCTTCTCCGCCGCCACCGACGTCAAACGAATCTCCTTCTCCTCCAGAA 334

Qy         60 ------------ProProSerProProThrProSerThrProGlySerProProPro--- 74
                        ||||||:::||||||      |||         :::|||||||||
Db        335 GATTCCGAAACACCACCTGCTCCACCAAATGAATCCAATGACAACAACCCTCCTCCGTCT 394

Qy         75 ------------LeuProGlnProSerProProAla------------ProThrThrPro 86
                           |||   ||||||   |||:::            ||||||   |||
Db        395 CAAGATCTTCAATCGCCTCCTCCATCGTCGCCGTCGCCGAATGTAGGACCCACAAACCCG 454

Qy         87 GlySerProPro------AlaProValThrProProThrArgAsnPro---------Pro 101
              |||||||||      :::|||      ||||||      :::|||         |||
Db        455 GAATCACCACCGTTACAATCTCCTCCAGCTCCACCAGCATCAGATCCTACAAATTCACCG 514

Qy        102 ProSerValProGlyProProSerAsnPro---------SerArgGluGlyGlySerPro 118
              |||:::   |||      |||:::||||||                    |||   :::
Db        515 CCAGCTTCACCATTAGACCCTACCAATCCTCCCCCAATACAACCATCAGGACCAGCCACT 574

Qy        119 ArgProProSerSerPro---SerProProSerPro---------------------- 129
                ||||||::::::|||   :::||||||||||||
Db        575 TCTCCTCCGGCTAATCCCAACGCTCCGCCGAGCCCATTCCCCACAGTACCACCCAAAACT 634

Qy        129 ------------------------------------------------------------ 129

Db        635 CCTTCTAGTGGACCTGTGGTGTCTCCATCTCTCACATCCCCTAGTAAAGGAACTCCTACT 694
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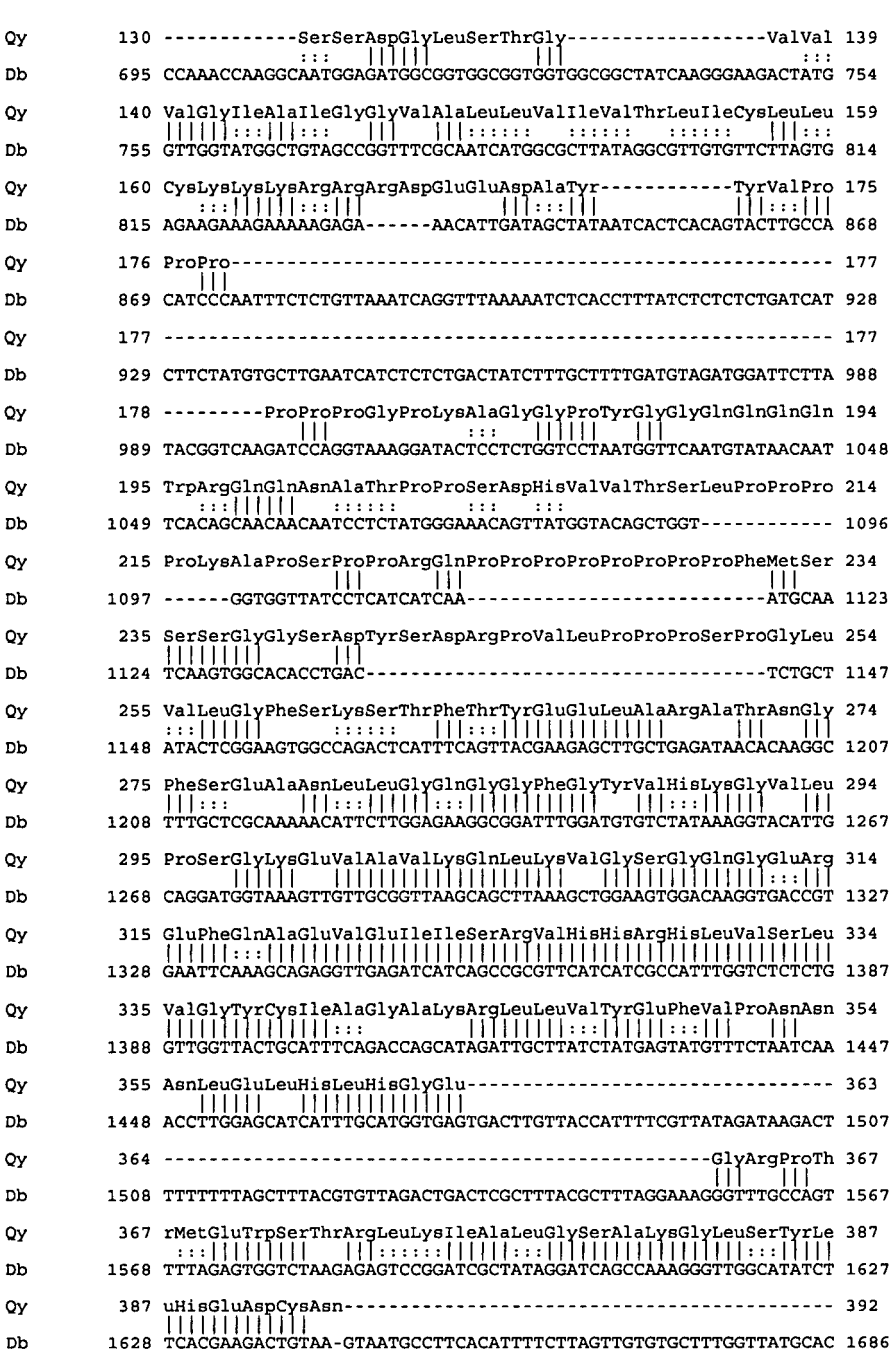
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Db 695 CCAAACCAAGGCAATGGAGATGGCGGTGGCGGTGGTGGCGGCTATCAAGGGAAGACTATG 754
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Db 755 GTTGGTATGGCTGTAGCCGGTTTCGCAATCATGGCGCTTATAGGCGTTGTGTTCTTAGTG 814
Qy 160 CysLysLysLysArgArgArgAspGluGluAspAlaTyr----------TyrValPro 175
Db 815 AGAAGAAAGAAAAAGAGA------AACATTGATAGCTATAATCACTCACAGTACTTGCCA 868
Qy 176 ProPro---------- 177
Db 869 CATCCCAATTTCTCTGTTAAATCAGGTTTAAAAATCTCACCTTTATCTCTCTCTGATCAT 928
Qy 177 ---------- 177
Db 929 CTTCTATGTGCTTGAATCATCTCTCTGACTATCTTTGCTTTTGATGTAGATGGATTCTTA 988
Qy 178 ---------ProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGln 194
Db 989 TACGGTCAAGATCCAGGTAAAGGATACTCCTCTGGTCCTAATGGTTCAATGTATAACAAT 1048
Qy 195 TrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuProProPro 214
Db 1049 TCACAGCAACAACAATCCTCTATGGGAAACAGTTATGGTACAGCTGGT---------- 1096
Qy 215 ProLysAlaProSerProProArgGlnProProProProProProProPheMetSer 234
Db 1097 ------GGTGGTTATCCTCATCATCAA----------ATGCAA 1123
Qy 235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeu 254
Db 1124 TCAAGTGGCACACCTGAC----------TCTGCT 1147
Qy 255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
Db 1148 ATACTCGGAAGTGGCCAGACTCATTTCAGTTACGAAGAGCTTGCTGAGATAACACAAGGC 1207
Qy 275 PheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294
Db 1208 TTTGCTCGCAAAAACATTCTTGGAGAAGGCGGATTTGGATGTGTCTATAAAGGTACATTG 1267
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Db 1268 CAGGATGGTAAAGTTGTTGCGGTTAAGCAGCTTAAAGCTGGAAGTGGACAAGGTGACCGT 1327
Qy 315 GluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeu 334
Db 1328 GAATTCAAAGCAGAGGTTGAGATCATCAGCCGCGTTCATCATCGCCATTTGGTCTCTCTG 1387
Qy 335 ValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 354
Db 1388 GTTGGTTACTGCATTTCAGACCAGCATAGATTGCTTATCTATGAGTATGTTTCTAATCAA 1447
Qy 355 AsnLeuGluLeuHisLeuHisGlyGlu---------- 363
Db 1448 ACCTTGGAGCATCATTTGCATGGTGAGTGACTTGTTACCATTTTCGTTATAGATAAGACT 1507
Qy 364 ----------GlyArgProTh 367
Db 1508 TTTTTTTAGCTTTACGTGTTAGACTGACTCGCTTTACGCTTTAGGAAAGGGTTTGCCAGT 1567
Qy 367 rMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLe 387
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Qy 387 uHisGluAspCysAsn---------- 392
Db 1628 TCACGAAGACTGTAA-GTAATGCCTTCACATTTTCTTAGTTGTGTGCTTTGGTTATGCAC 1686
Qy 393 ----------ProLy 394
Db 1687 TTCATAGTTTAAACAGAAGCCAAAAATCATATCCTTGTTTTATTTTACAGGTCATCCGAA 1746
Qy 394 sIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLy 414
Db 1747 AATCATTCACAGAGATATAAAGTCAGCAAATATTCTTCTAGATGATGAAATATGAAGCTCA 1806
Qy 414 s---------- 414
Db 1807 -GGCAATAATGAAATCCTCCTTTTCGTTAAATCTATCTTATGACTGTAAAGTTTTAGTTA 1865
Qy 415 ----------ValAlaAspPheGlyLeuAlaLysIleAl 424
Db 1866 ATGAGACTTGTTCTGTTTTTTGGATGTTTAGGTTGCTGATTTTGGACTTGCTAGACTCAA 1925
Qy 424 aSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe-Gly---------- 440
Db 1926 TGATACAACACAAACTCATGTTTCAACTCGGGTTATGGGAACCTTCGGGTAAGCAAACAT 1985
Qy 440 ---------- 440
Db 1986 TCATCACAAACTCTACTCCAAAACTGGACCTTATTGATCCAATGCCTGATGAAAAGTTTG 2045
Qy 440 ---------- 440
Db 2046 TTATATATGGCTTGAGGCAACAAATTGGATCAAACCTGAATCTTTATTGATCGTATGGCT 2105
Qy 441 ----------TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuT 453
Db 2106 GCATGACATGTTTTGTGTTAAGGTACCTAGCGCCGGAATATGCATCAAGTGGAAAATTGA 2165
Qy 453 hrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgA 473
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Qy 473 rgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp---------- 489
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Db 2346 TAAATGAACTCACAGGCGCGCCCGCTGCTTCTCAAAGCCATTGAGACCGGAGATTTAAGC 2405
Qy 505 GlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVal 524
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Qy 525 AlaCysAlaAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGln--- 543
Db 2466 GAGACAGCCGCTGCATGTGTTAGACATTCTGGTCCAAAACGCCCACGCATGGTTCAGGTA 2525
Qy 543 ---------- 543
Db 2526 ATTCTGACTAACCAAAAGTCCAAAGCTCCCATATATAGTAACAAGTGATTTCTCACATCT 2585
Qy 544 ----------IleValArgAlaLeuGluGlyAsnValSerLeu 554
Db 2586 GAAAACTTATCTACTCTTCGAAATAAGGTTGTGAGAGCATTGGACTGCGACGGAGACTCG 2645
Qy 555 SerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGly 574
Db 2646 GGAGATATTAGCAACGGAATCAAAATTGGGCAA---------- 2678
Qy 575 SerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAla 594
Db 2679 AGCACAACTTATGACTCAGGGCAATACAATGAAGACATTATGAAATTCAGGAAAATGGCG 2738
Qy 595 LeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGly 614

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Db       2739 TTTGGTGGTGATAACAGCGTAGAGTCAGGATTGTACAGT-----------------GGA 2780

Qy        615 LeuTyrProSerGlySerSerSerGlu 623
                ||| |:::  |||||||||:::
Db       2781 AACTACTCTGCCAAAAGCTCTTCAGAT 2807

RESULT 15
ACF36553
ID   ACF36553 standard; DNA; 3060 BP.
XX
AC   ACF36553;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Arabidopsis PERK1 receptor related protein encoding DNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82942.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 14; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a PERK1 polypeptide related protein encoding genomic
CC   DNA from A. thaliana (Accession NO. CAA18590)
XX
SQ   Sequence 3060 BP; 797 A; 766 C; 592 G; 905 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.1e-27         Length:         3060
Score:                  1185.00         Matches:        342
Percent Similarity:     39.28%          Conservative:   72
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US-10-086-464-2 (1-647) x ACF36553 (1-3060)
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Qy          2 SerSerAlaProSerProGlyThrGlySerProPro----------------------- 13
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Qy         14 -----------------SerProProSerAsnSerThrThrThrThrProProProAla 27
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Db        100 TCCGTACCTGACACGTCATCACCTCCAGCTCCTCCTTTGTCTCCTCTTCCCCCACCATTG 159

Qy         28 SerAlaProProProThrThrProSerSerProPro----------------------- 39
              |||:::|||||||||      ||||||  ||||||
Db        160 AGCTCTCCTCCGCCG---TTGCCTTCACCACCGCCTCTCTCCGCTCCCACCGCTTCCCCA 216

Qy         40 ---------------------ProProSerThrIleProThrSerProProProSerSer 52
                                   |||||||||           ||||||||||||
Db        217 CCGCCTCTTCCGGTTGAATCCCCACCGTCTCCTCCTATAGAATCACCACCGCCTCCTCTA 276

Qy         53 ArgSerThrProSerAlaProPro---------ProSerProProThrPro------Ser 67
                 :::|||      ||||||          ||||||||||||:::|||      |||
Db        277 CTGGAATCACCTCCTCCTCCTCCGTTGGAATCTCCATCTCCACCGTCTCCTCACGTCTCA 336

Qy         68 ThrProGlySerProProProLeuPro-----------GlnProSerProProAlaPro 83
              |||         ||||||||||||              :::||||||||||||
Db        337 GCTCCTTCCGGTTCACCGCCATTACCCTTCCTTCCCGCCAAACCTTCTCCGCCG------ 390

Qy         84 ThrThrProGlySerProProAlaProValThrProPro------ThrArgAsnProPro 101
                 |||  |||||||||:::          ||||||      |||   :::||||||
Db        391 ------CCTTCTTCACCTCCCTCCGAGACAGTTCCGCCGGGAAATACGATTTCTCCACCA 444

Qy        102 Pro---------------------------------------SerValProGlyProPro 108
              |||                                      :::   |||   ||||||
Db        445 CCTCGTTCACTTCCCTCCGAATCAACCCCGCCGGTGAACACAGCTTCTCCTCCACCGCCA 504

Qy        109 SerAsnProSerArgGluGlyGlySerProArgPro----------------------- 120
              |||   |||   |||      |||   |||:::|||
Db        505 TCTCCTCCTCGCCGCCGTAGTGGC---CCTAAGCCTTCGTTTCCTCCTCCCATCAATTCT 561

Qy        121 ---ProSerSerProSerPro-------------------------------------- 126
                 |||   :::|||||||||
Db        562 TCTCCACCAAATCCTTCTCCGAACACTCCGTCACTCCCAGAAACTTCTCCTCCACCTAAA 621

Qy        127 ------------------ProSerProSerSer------------------------- 131
                               |||   |||||||||
Db        622 CCACCGCTCTCAACGACGCCATTTCCCTCCTCATCCACTCCCCCGCCTAAGAAGTCCCCT 681

Qy        132 ---------------------------------------------AspGlyLeu------ 134
                                                          ||||||
Db        682 GCAGCAGTAACTCTTCCTTTCTTTGGGCCAGCGGGCCAATTACCGGATGGGACCGTAGCA 741

Qy        134 ------------------------------------------------------------ 134

Db        742 CCTCCTATTGGGCCTGTTATAGAGCCCAAGACGAGTCCAGCCGAATCAATATCTCCGGGA 801

Qy        135 ------------------------------------------------------------ 135

Db        802 ACGCCACAGCCACTGGTTCCGAAGAGTCTACCTGTAACGACGTCGTATCACCGATCATCC 861

Qy        136 ThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeu 155
                 |||   :::   |||      |||   |||      ||||||:::::::::   |||
Db        862 GCCGGATTCTTATTTGGCGGTGTAATCGTTGGAGCTCTTCTACTAATTCTGTTAGGTCTT 921

Qy        156 IleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAsp-AlaTyrTyrValPr 175
              :::   :::      :::      |||   |||:::          |||      :::
Db        922 CTCTTTGTCTTCTACAGAGCTACCAGAAATAGAAATAACAACAGCAGCTCTGCTCATCAT 981

Qy        175 oProProProProPro------------------------------------------- 180
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Db        982 CAATCCAAAACTCCCTCAAAAGGTATAAACTTTGAGATCAATTTGTTTCAGACTGTCACT 1041

Qy        181 ------------GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpAr 196
                          |||                  |||      |||      ||
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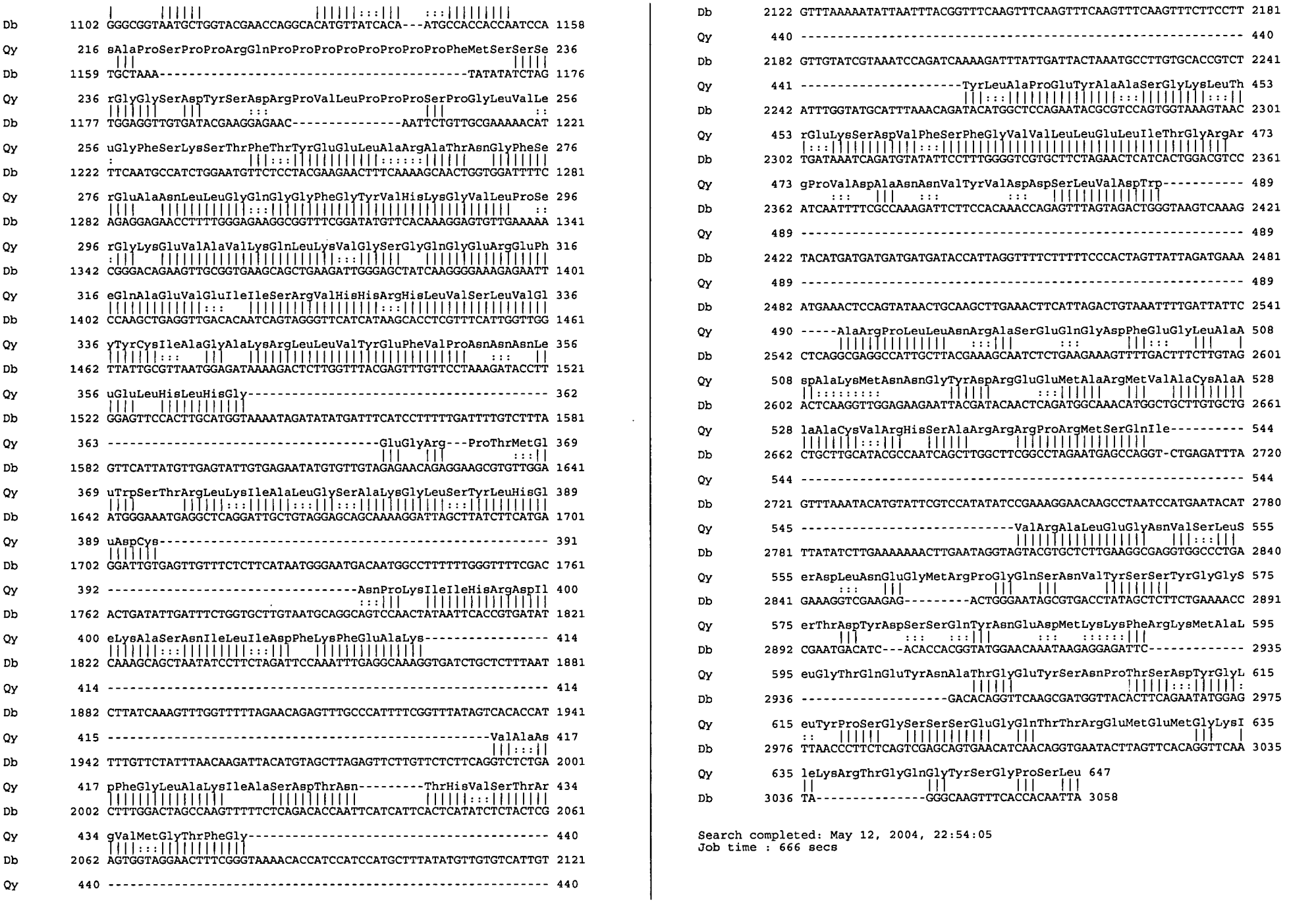

Search completed: May 12, 2004, 22:54:05
Job time : 666 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2004, 22:25:16 ; Search time 3599 Seconds
(without alignments)
5368.389 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estin:*
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7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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19: em_gss_pln:*
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25: em_gss_rod:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1092.5	31.6	1084	12	BP184771	BP184771 BP184771
2	1090.5	31.6	824	14	CD435142	CD435142 EL01N0355
3	1086	31.5	788	14	CF436437	CF436437 EST672782
4	1071	31.0	789	14	CF436655	CF436655 EST673000
5	1069	31.0	759	12	BM408099	BM408099 EST582426
6	1066	30.9	785	14	CF436122	CF436122 EST672467
7	1065	30.8	757	12	BG596561	BG596561 EST495239
8	1063	30.8	731	14	CB655196	CB655196 OSJNEc08F
9	1047	30.3	692	12	BG441204	BG441204 GA__Ea001
10	1030	29.8	723	14	CD839231	CD839231 RFO2.114I
11	1027.5	29.8	1053	11	AY108241	AY108241 Zea mays
12	1025	29.7	1016	11	AY108243	AY108243 Zea mays
13	1018	29.5	666	12	BM358715	BM358715 GA__Ea001
14	1013	29.3	695	13	CA072174	CA072174 SCCCAM100
15	983	28.5	715	13	BU099573	BU099573 WHE3309_A
16	961	27.8	770	13	BQ999193	BQ999193 QGG21G04.
17	931	27.0	611	14	CA237156	CA237156 SCMCFL500
c 18	931	27.0	859	29	CC725849	CC725849 OGGAB66TC
19	929.5	26.9	809	14	CA765135	CA765135 AF53-Rpf_
20	928	26.9	850	29	CC668754	CC668754 OGGAB66TM
c 21	923.5	26.7	769	14	CK283399	CK283399 EST746121
22	921	26.7	618	14	CA269355	CA269355 SCBGRT307
23	921	26.7	651	14	CF478389	CF478389 RTWW3_18_
24	920	26.6	673	14	CA164704	CA164704 SCSBRZ312
c 25	919.5	26.6	938	29	CG333846	CG333846 OG0GA30TV
c 26	917.5	26.6	949	29	CG436431	CG436431 OGVGH77TV
27	912	26.4	679	13	BQ404121	BQ404121 GA__Ed006
28	904.5	26.2	674	14	CA298046	CA298046 SCMCFL802
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31	903	26.2	645	13	BQ506869	BQ506869 EST614284
c 32	897.5	26.0	899	14	CK096498	CK096498 UB16CPE10
33	895.5	25.9	682	13	CA095337	CA095337 SCCCCL500
34	895	25.9	641	14	CA248316	CA248316 SCCCFL509
c 35	895	25.9	725	29	CG450877	CG450877 OG7AK95TH
c 36	893.5	25.9	803	14	CF243440	CF243440 3530_1_21
37	891	25.8	646	13	BQ240617	BQ240617 TaE05015B
38	891	25.8	652	13	BQ849683	BQ849683 QGB10I20.
39	891	25.8	666	13	BU499754	BU499754 946178G10
40	891	25.8	691	14	CA237152	CA237152 SCMCFL500
41	889	25.7	626	13	BQ582873	BQ582873 E012278-0
42	888.5	25.7	593	10	BF176907	BF176907 EM1_4_B10
43	887	25.7	622	14	CA999610	CA999610 S345P_H09
44	887	25.7	673	13	BQ410602	BQ410602 GA__Ed003
45	886.5	25.7	573	9	AV551753	AV551753 AV551753

ALIGNMENTS

RESULT 1
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LOCUS BP184771 1084 bp mRNA linear EST 17-JUL-2003
DEFINITION BP184771 pNS rice panicle cDNA, germ cell generating stage Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.
ACCESSION BP184771
VERSION BP184771.1 GI:32948199
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

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REFERENCE   1  (bases 1 to 1084)
  AUTHORS   Moriguchi,K., Ito,Y., Yamazaki,Y. and Kurata,N.
  TITLE     Finding of various plant nuclear proteins using yeast nuclear
            transportation trap system - a proteomal approach
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Kazuki Moriguchi
            Plant Genetics
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-55-981-6872
            Fax: 81-55-981-6879
            Email: kmoriguc@lab.nig.ac.jp
            cDNA clone obtained from nuclear transportation trap system
            encoding a protein similar to Oryza sativa (japonica
            cultivar-group) putative receptor protein kinase PERK1.
FEATURES             Location/Qualifiers
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ORIGIN

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Query Match:            31.64%          Indels:         7
DB:                     12              Gaps:           3

US-10-086-464-2 (1-647) x BP184771 (1-1084)

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
              |||||||||:::||||||||||||||||||||   ||||||||||||||||||||||||
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Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
              :::||||||||||||:::||||||||||||||||:::||||||||||||||||||||||
Db         62 GCTGCAAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCTAAGATCATCCATCGTGAT 121

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419
              ||||||||||||||||||:::||||||||||||||:::||||||||||||||||||||
Db        122 ATTAAGGCGTCAAACATTCTTCTTGATTTTAAGTTTGAATCTAAGGTTGCTGATTTTGGA 181

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              |||||||||      ||||||   ||||||||||||||||||||||||||||||||||||
Db        182 CTTGCTAAGTTCACCAGTGATAATAACACTCATGTTTCGACAAGAGTAATGGGCACTTTT 241

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        242 GGATATCTAGCACCAGAGTACGCATCTTCTGGCAAGCTCACTGAGAAATCAGATGTCTTC 301

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
              |||:::||||||:::||||||||||||||||||||||||||||||||||   :::
Db        302 TCCTATGGAGTTATGCTTCTTGAGTTAATAACTGGTCGTCGGCCAGTTGATACAAGTCAA 361

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
              |||:::||||||||||||||||||||||||||||||||||||   :::|||   |||
Db        362 ACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCTTTACTGATGCAAGCACTTGAG 421

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
              |||:::::|||   |||   |||   ::::::         ::::::      |||
Db        422 AATGGTAACTACGAGGAGTTAGTAGATCCTCGGCTTGGGAAGGATTTCAATCCCAATGAG 481

Qy        520 MetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPro 539
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        482 ATGGCGAGAATGATTGCTTGTGCAGCTGCATGCGTACGCCATTCCGCTCGTCGTCGCCCA 541

Qy        540 ArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGlu 559
              ||||||||||:::||||||||||||||||||||:::|||||||||   ||||||||||
Db        542 CGCATGAGCCAGGTTGTCCGGGCTTTGGAAGGTGACGTGTCTTTGGAGGATCTTAATGAA 601

Qy        560 GlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAsp 579
              |||:::||||||||   |||     :::   ||||||      |||:::||||||||||
Db        602 GGTGTTCGGCCTGGTCACAGCCGCTATTTTGGATCGTAC---AGCAGCTCTGACTATGAT 658

Qy        580 SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGlu 599
              |||   ||||||||||||||||||||||||||||||||||||||||||      |||
Db        659 TCTGGCCAATACAACGAGGACATGAAGAAGTTCAGGAAGATGGCTTTT---ACCAACAAT 715

Qy        600 TyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGly 619
                  :::   :::   :::||||||   |||||||||:::||||||      ||||||
Db        716 AATGATACGAGCAGTCAATACAGCGCACCAACCAGCGAGTATGGCCAGATACCCTCTGCA 775

Qy        620 SerSerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly 639
              ||||||||||||||||||   |||:::|||:::|||                ||||||   |||
Db        776 TCAAGCAGCGAGGGCCAACAAACCCAGGAAGTCGAGAGCAGGACAACCAAGAGAGGCGGC 835

Qy        640 --------------GlnGlyTyrSerGlyProSer 646
                             ||||||||||||   |||
Db        836 TACAGTGGCTACAGCTCAGGATACAGCGGAGCCTCA 871

RESULT 2
CD435142
LOCUS       CD435142                824 bp    mRNA    linear   EST 03-JUN-2003
DEFINITION  EL01N0355D03.b Endosperm_3 Zea mays cDNA, mRNA sequence.
ACCESSION   CD435142
VERSION     CD435142.1  GI:31350785
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 824)
  AUTHORS   Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
            Messing,J.
  TITLE     Sequencing of the maize endosperm ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Lai, Jinsheng
            Dr. Joachim Messing's lab
            Waksman Institute, Rutgers University
            190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
            Tel: 732-445-3801
            Fax: 732-445-5735
            Email: jlai@waksman.rutgers.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
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ORIGIN

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US-10-086-464-2 (1-647) x CD435142 (1-824)

Qy        334 LeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsn 353
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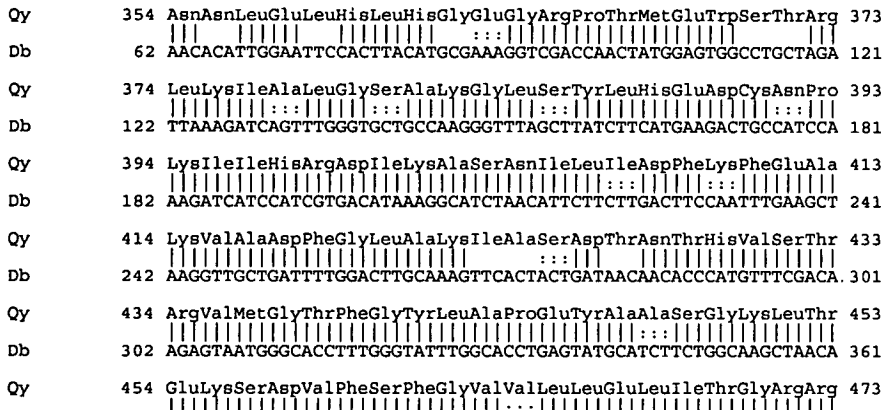

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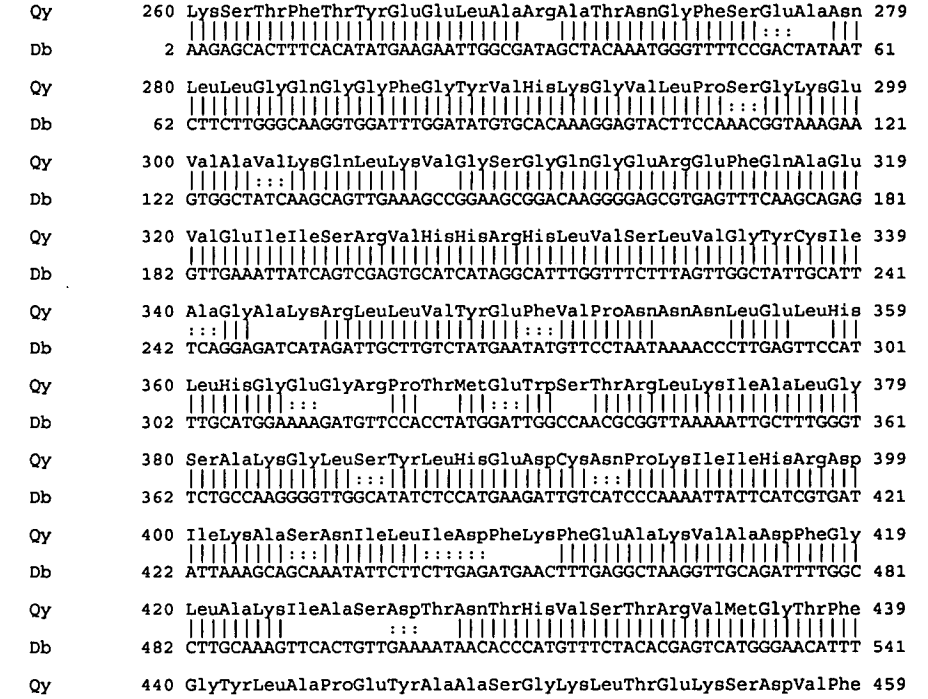
CF436437
LOCUS CF436437 788 bp mRNA linear EST 04-SEP-2003
DEFINITION EST672782 normalized cDNA library of onion Allium cepa cDNA clone ACACM44, mRNA sequence.
ACCESSION CF436437
VERSION CF436437.1 GI:34459127
KEYWORDS EST.
SOURCE Allium cepa (onion)
ORGANISM Allium cepa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
REFERENCE 1 (bases 1 to 788)
AUTHORS Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
TITLE Expressed Sequence Tags from a normalized library of mixed onion tissues (Allium cepa)
JOURNAL Unpublished (2003)
COMMENT Contact: Havey MJ
Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA
Tel: 608-262-1830
Fax: 608-262-4743
Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACACM44TR. For more information:
http://haveylab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES Location/Qualifiers
source 1. .788
/organism="Allium cepa"
/mol_type="mRNA"
/cultivar="Red Creole(bulbs), unknown(callus), Ebano & Texas Legend(roots)"
/db_xref="taxon:4679"
/clone="ACACM44"
/tissue_type="Callus, roots, and young bulbs"
/clone_lib="normalized cDNA library of onion"
/note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1: EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA from callus, roots, and young bulbs were combined to synthesize the library. Normalization to enrich for low-copy transcripts was performed by proprietary techniques of Invitrogen."
ORIGIN

Alignment Scores:

Pred. No.:	6.07e-26	Length:	788
Score:	1086.00	Matches:	204
Percent Similarity:	87.79%	Conservative:	26
Best Local Similarity:	77.86%	Mismatches:	32
Query Match:	31.45%	Indels:	0
DB:	14	Gaps:	0

US-10-086-464-2 (1-647) x CF436437 (1-788)



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Db        542 GGGTATCTGGCACCAGAATATGCATCCTCTGGTAAACTAAGTGATAAATCAGATGTCTTT 601

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479

Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499

Db        662 ACTTATACAGATGATAGTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGAG 721

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519

Db        722 CATGATGATTATGATGAGCTCATTGACAGAAGGCTAGGAGATAAATACAACCATGACGAA 781

Qy        520 MetAla 521

Db        782 ATGGCA 787

RESULT 4
CF436655
LOCUS       CF436655                789 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST673000 normalized cDNA library of onion Allium cepa cDNA clone
            ACACK26, mRNA sequence.
ACCESSION   CF436655
VERSION     CF436655.1  GI:34459345
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 789)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACACK26TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .789
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACACK26"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

Alignment Scores:
Pred. No.:              1.82e-25      Length:         789
Score:                  1071.00       Matches:        203
Percent Similarity:     86.64%        Conservative:   24
Best Local Similarity:  77.48%        Mismatches:     35
Query Match:            31.02%        Indels:         0
DB:                     14            Gaps:           0
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US-10-086-464-2 (1-647) x CF436655 (1-789)

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279

Db          2 AAGAGCACTTTCACATATGAAGAATTGGCGATAGCTACAAATGGGTTTTCCGACTATAAT 61

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGlu 299

Db         62 CTTCTTGGGCAAGGTGGATTTGGATATGTGCACAAAGGAGTACTTCCAAACGGTAAAGAA 121

Qy        300 ValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGlu 319

Db        122 GTGGCTATCAAGCAGTTGAAAGCCGGAAGCGGACAAGGGGAGCGTGAGTTTCAAGCAGAG 181

Qy        320 ValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIle 339

Db        182 GTTGAAATTATCAGTCGAGTGCATCATAGGCATTTGGTTTCTTTAGTTGGCTATTGCATT 241

Qy        340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHis 359

Db        242 TCAGGAGATCATAGATTGCTTGTCTATGAATATGTTCCTAATAAAACCCTTGAGTTCCAT 301

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379

Db        302 TTGCATGGAAAAGATGTTCCACCTATGGATTGGCCAACGCGGTTAAAAATTGCTTTGGGT 361

Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399

Db        362 TCTGCCAAGGGGTTGGCATATCTCCATGAAGATTGTCATCCCAAAATTATTCATCGTGAT 421

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419

Db        422 ATTAAAGCAGCAAATATTCTTCTTGAGATGAACTTTGAGGCTAAGGTTGCAGATTTTGGC 481

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439

Db        482 CTTGCAAAGTTCACTGTTGAAAATAACACCCATGTTTCTACACGAGTCATGGGAACATTT 541

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459

Db        542 GGGTATCTGGCACCAGAATATGCATCCTCTGGTAAACTAAGTGATAAATCAGATGTCTTT 601

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479

Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499

Db        662 ACTTATACAGATGATAGTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGAG 721

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519

Db        722 CATGATGATTATGATGAGCTCATTGACAGAAGGCTAGGAGATAAATACCACCCATGACGA 781

Qy        520 MetAla 521

Db        782 ATGGCA 787

RESULT 5
BM408099
LOCUS       BM408099                759 bp    mRNA    linear   EST 10-MAR-2003
DEFINITION  EST582426 potato roots Solanum tuberosum cDNA clone cPRO33O21 5'
            end, mRNA sequence.
ACCESSION   BM408099
VERSION     BM408099.1  GI:18259729
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   van der Hoeven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
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            Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
            Tanksley,S. and Baker,B.
  TITLE     Generation of ESTs from potato roots
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cPRO33021"
                     /tissue_type="roots"
                     /dev_stage="in vitro grown stem cuttings"
                     /lab_host="SOLR"
                     /clone_lib="potato roots"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Cornell University, Tanksley lab;
                     sequencing; The Institute for Genomic Research. Roots were
                     isolated from in vitro grown stem cuttings on CM medium.
                     Roots were isolated two weeks after placing the stem
                     cuttings from in vitro grown plants on medium."
ORIGIN

Alignment Scores:
Pred. No.:              2.04e-25        Length:         759
Score:                  1069.00         Matches:        200
Percent Similarity:     89.29%          Conservative:   25
Best Local Similarity:  79.37%          Mismatches:     27
Query Match:            30.96%          Indels:         0
DB:                     12              Gaps:           0

US-10-086-464-2 (1-647) x BM408099 (1-759)

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db          2 GGGGAACGTGAATTTCAGGCGGAAGTTGAGATTATTAGCCGAGTACATCACAAGCATCTT 61

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351
              ||||||||||||||||||||||||    |||||||:::||||||||||||||||||||||
Db         62 GTGTCTCTTGTTGGATACTGCATTACTGGGGCTCAGAGACTGCTTGTTTATGAGTTTGTT 121

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371
              |||||||||    ||||||   ||||||||||||:::|||||||||    ::::::|||
Db        122 CCAAACAATACTTTGGAATTTCATTTACACGGAAAGGGAAGGCCTCCTTTGGATTGGCCA 181

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        182 ATACGGCTAAAGATTGCTCTAGGGTCAGCTAAAGGACTGGCATATCTGCATGAAGACTGC 241

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411
              ||||||||||||||||||||||||||||||:::|||||||||||||||||    |||
Db        242 CAACCGAAAATCATTCACCGTGATATCAAGGCAGCTAATATACTTATCGACTTTAATTTT 301

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisVal 431
              ||||||||||||||||||||||||||||||:::    ||||||    ||||||||||||
Db        302 GAGGCTAAGGTTGCTGATTTTGGACTTGCCAAGCTAACTTCTGATGTTAATACTCATGTC 361

Qy        432 SerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLys 451
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||
Db        362 TCCACCAGAGTGATGGGAACCTTTGGGTATTTGGCTCCAGAATATGCTTCCTCTGGAAAG 421

Qy        452 LeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGly 471
              ||||||:::||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        422 CTTACAGACAAGTCAGACGTATTCTCCTTTGGTGTAATGCTTCTTGAGTTGATAACTGGA 481

Qy        472 ArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArg 491
              ||||||||||||||:::          |||:::::|||||||||||||||||||||||||
Db        482 CGTCGGCCTGTTGACTCTACTCAATCATACATCGAAGATAGTTTGGTGGACTGGGCACGT 541

Qy        492 ProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMet 511
              |||||||||   ||||||   |||          |||:::   |||   |||   ::::::
Db        542 CCATTACTCACACGAGCTTTAGAAGATGAAAAGTTTGATACCCTTGTTGATCGTCGGCTA 601

Qy        512 AsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVal 531
                  |||   |||:::      ||||||||||||||||||||||||   ||||||||||||
Db        602 GAAAATGATTATAACCATAATGAGATGGCTCGCATGGTTGCTTGTTGTGCTGCTTGTGTG 661

Qy        532 ArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsn 551
              ||||||||||||:::||||||||||||||||:::|||:::::|||||||||||||||:::
Db        662 CGTCATTCAGCAAAGCGTAGACCACGAATGACACAGGTTCTCCGAGCCTTGGAAGGAGAT 721

Qy        552 ValSerLeuSerAspLeuAsnGluGlyMetArgPro 563
              ||||||||||||||||||   ||||||:::::|||
Db        722 GTCTCATTATCAGACCTTTACGAAGGGATTAAACCT 757

RESULT 6
CF436122
LOCUS       CF436122                785 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  EST672467 normalized cDNA library of onion Allium cepa cDNA clone
            ACACJ26, mRNA sequence.
ACCESSION   CF436122
VERSION     CF436122.1  GI:34458812
KEYWORDS    EST.
SOURCE      Allium cepa (onion)
  ORGANISM  Allium cepa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
            Allium.
REFERENCE   1  (bases 1 to 785)
  AUTHORS   Havey,M.J., Cheung,F., Van Aken,S., Utterback,T. and Town,C.D.
  TITLE     Expressed Sequence Tags from a normalized library of mixed onion
            tissues (Allium cepa)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Havey MJ
            Department of Horticulture
            USDA-ARS and University of Wisconsin
            1575 Linden Drive, Madison, WI 53706, USA
            Tel: 608-262-1830
            Fax: 608-262-4743
            Email: mjhavey@facstaff.wisc.edu
            TIGR sequence name ACACJ26TR. For more information:
            http://haveylab.hort.wisc.edu
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .785
                     /organism="Allium cepa"
                     /mol_type="mRNA"
                     /cultivar="Red Creole(bulbs), unknown(callus), Ebano &
                     Texas Legend(roots)"
                     /db_xref="taxon:4679"
                     /clone="ACACJ26"
                     /tissue_type="Callus, roots, and young bulbs"
                     /clone_lib="normalized cDNA library of onion"
                     /note="Vector: pCMVSport6.1-ccdb (Invitrogen); Site_1:
                     EcoRV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
                     from callus, roots, and young bulbs were combined to
                     synthesize the library. Normalization to enrich for
                     low-copy transcripts was performed by proprietary
                     techniques of Invitrogen."
ORIGIN

Alignment Scores:
Pred. No.:              2.61e-25        Length:         785
Score:                  1066.00         Matches:        204
Percent Similarity:     86.64%          Conservative:   23
Best Local Similarity:  77.86%          Mismatches:     34
Query Match:            30.87%          Indels:         1
DB:                     14              Gaps:           0
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US-10-086-464-2 (1-647) x CF436122 (1-785)

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
              ||||||||||||||||||||||||||||||   ||||||||||||||||||:::   |||
Db          2 AAGAGCACTTTCACATATGAAGAATTGGCGATAGCTACAAATGGGTTTTCCGACTATAAT 61

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGlu 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db         62 CTTCTTGGGCAAGGTGGATTTGGATATGTGCACAAAGGAGTACTTCCAAACGGTAAAGAA 121

Qy        300 ValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGlu 319
              ||||||:::||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        122 GTGGCTATCAAGCAGTTGAAAGCCGGAAGCGGACAAGGGGAGCGTGAGTTTCAAGCAGAG 181

Qy        320 ValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIle 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTTGAAATTATCAGTCGAGTGCATCATAGGCATTTGGTTTCTTTAGTTGGCTATTGCATT 241

Qy        340 AlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHis 359
              :::|||      |||||||||||||||||:::|||||||||      ||||||   |||
Db        242 TCAGGAGATCATAGATTGCTTGTCTATGAATATGTTCCTAATAAAACCCTTGAGTTCCAT 301

Qy        360 LeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGly 379
              |||||||||:::      |||   |||:::|||   |||||||||||||||||||||||
Db        302 TTGCATGGAAAAGATGTTCCACCTATGGATTGGCCAACGCGGTTAAAAATTGCTTTGGGT 361

Qy        380 SerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAsp 399
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Db        362 TCTGCCAAGGGGTTGGCATATCTCCATGAAGATTGTCATCCCAAAATTATTCATCGTGAT 421

Qy        400 IleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGly 419
              ||||||||||:::|||||||||::::::      ||||||||||||||||||||||||||
Db        422 ATTAAAGCAGCAAATATTCTTCTTGAGATGAACTTTGAGGCTAAGGTTGCAGATTTTGGC 481

Qy        420 LeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              |||||||||         :::   ||||||||||||||||||||||||||||||||||||
Db        482 CTTGCAAAGTTCACTGTTGAAAATAACACCCATGTTTCTACACGAGTCATGGGAACATTT 541

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
              ||||||||||||||||||||||:::||||||||||||::::::||||||||||||||||
Db        542 GGGTATCTGGCACCAGAATATGCATCCTCTGGTAAACTAAGTGATAAATCAGATGTCTTT 601

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
              ||||||||||:::|||||||||||||||||||:::|||||||||||||||||
Db        602 TCATTTGGAGTCATGCTTTTGGAGCTGATTACTGGAAAGCGACCAGTTGATGCAACCCAA 661

Qy        480 ValTyrValAspAspSer-LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGl 499
              |||   |||||||| ||||||||||||||||||||||||   :::|||   ||
Db        662 ACTTATACAGATGATAGTTTTGGTCGATTGGGCAAGACCATTGCTGCAGAAGGCTATGGA 721

Qy        499 uGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGl 519
              |      |||::::::   |||   |||   |||          |||:::   :::||
Db        722 GCATGATGATTATGATGAGCTCATTGACAGAAAGGCTAGGAGATAATACAACCATGACGA 781

Qy        519 uMet 520
              ||||
Db        782 AATG 785

RESULT 7
BG596561
LOCUS       BG596561                757 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST495239 cSTS Solanum tuberosum cDNA clone cSTS15A23 5' sequence,
            mRNA sequence.
ACCESSION   BG596561
VERSION     BG596561.1  GI:13614701
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from sprouting potato eyes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .757
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTS15A23"
                     /tissue_type="sprouting eyes from tubers"
                     /dev_stage="12-14 weeks post harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTS"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
                     taken from tubers. The tubers were incubated at 26C in the
                     dark for 2-3 weeks prior to sprouting. The eyes were
                     frozen in liquid nitrogen immediately upon removal from
                     tubers."
ORIGIN

Alignment Scores:
Pred. No.:              2.72e-25        Length:         757
Score:                  1065.00         Matches:        200
Percent Similarity:     89.16%          Conservative:   22
Best Local Similarity:  80.32%          Mismatches:     27
Query Match:            30.84%          Indels:         0
DB:                     12              Gaps:           0

US-10-086-464-2 (1-647) x BG596561 (1-757)

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db          1 GCAGTTAAACAGCTTAAGGCTGGAAGTGGACAAGGGGAACGTGAATTTCAGGCGGAAGTT 60

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db         61 GAGATTATTAGCCGAGTACATCACAAGCATCTTGTGTCTCTTGTTGGATACTGCATTACT 120

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||:::||||||||||||||||||||||||||||||   ||||||   ||||||
Db        121 GGGGCTCAGAGACTGCTTGTTTATGAGTTTGTTCCAAACAATACTTTGGAATTTCATTTA 180

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||:::||||||||||   ::::::|||       ||||||||||||||||||||||
Db        181 CACGGAAAGGGAAGGCCTCCTTTGGATTGGCCAATACGGCTAAAGATTGCTCTAGGGTCA 240

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||:::||||||||||||||||||   ||||||||||||||||||||||||||
Db        241 GCTAAAGGACTGGCATATCTGCATGAAGACTGCCAACCGAAAATCATTCACCGTGATATC 300

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||:::||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        301 AAGGCAGCTAATATACTTATCGACTTTAATTTTGAGGCTAAGGTTGCTGATTTTGGACTT 360

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||:::   ||||||   ||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAGCTAACTTCTGATGTTAATACTCATGTCTCCACCAGAGTGATGGGAACCTTTGGG 420

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||:::||||||||||||||:::||||||||||||||||||||||
Db        421 TATTTGGCTCCAGAATATGCTTCCTCTGGAAAGCTTACAGACAAGTCAGACGTATTCTCC 480
```

```
Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||:::|||||||||||||||||||||||||||||||||||||||||:::
Db        481 TTTGGTGTAATGCTTCTTGAGTTGATAACTGGACGTCGGCCTGTTGACTCTACTCAATCA 540

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              |||::::::|||||||||||||||||||||||||||||||||    ||||||   |||
Db        541 TACATCGAAGATAGTTTGGTGGACTGGGCACGTCCATTACTCACACGAGCTTTAGAAGAT 600

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
                  |||:::   |||   |||   ::::::   |||   |||:::          ||||||
Db        601 GAAAAGTTTGATACCCTTGTTGATCGTCGGCTAGAAAATGATTATAACCATAATGAGATG 660

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||   ||||||||||||||||||||:::|||||||||||||
Db        661 GCTCGCATGGTTGCTTGTTGTGCTGCTTGTGTGCGTCATTCAGCAAAGCGTAGACCACGA 720

Qy        541 MetSerGlnIleValArgAlaLeuGlu 549
              |||:::|||::::::||||||||||||
Db        721 ATGACACAGGTTCTCCGAGCCTTGGAA 747

RESULT 8
CB655196
LOCUS       CB655196                731 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  OSJNEc08F21.f OSJNEc Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNEc08F21 5', mRNA sequence.
ACCESSION   CB655196
VERSION     CB655196.1  GI:29658921
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 731)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 08  row: F  column: 21
            Seq primer: gta aaa cga cgg cca gtg.
FEATURES             Location/Qualifiers
     source          1. .731
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /clone="OSJNEc08F21"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSJNEc"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                     XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
ORIGIN

Alignment Scores:
Pred. No.:              3.05e-25        Length:         731
Score:                  1063.00         Matches:        199
Percent Similarity:     91.36%          Conservative:   23
Best Local Similarity:  81.89%          Mismatches:     21
Query Match:            30.78%          Indels:         0

DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x CB655196 (1-731)

Qy        311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db          1 CAGGGAGAGCGTGAATTCCAGGCGGAGGTTGAGATTATCAGCAGAGTACATCACAAACAT 60

Qy        331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
              ||||||||||||||||||||||||||:::|||   ||||||||||||||||||||||
Db         61 CTCGTCTCCTTGGTTGGTTATTGCATTTCTGGGGGCAAGAGATTGCTTGTCTATGAGTTT 120

Qy        351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              ||||||||||||   ||||||   ||||||||||||:::||||||||||||||||||||
Db        121 GTCCCCAACAACACATTGGAATTCCACTTGCACGGAAAAGGCCGACCAACAATGGAGTGG 180

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
              ||||||||||||||||||||||:::|||||||||||||:::||||||||||||||||||
Db        181 CCCACAAGACTAAAGATTGCTTTGGGAGCTGCAAAGGGTTTAGCTTATCTTCATGAAGAC 240

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::|||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        241 TGCCATCCTAAGATCATCCATCGTGATATTAAGGCGTCAAACATTCTTCTTGATTTTAAG 300

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||:::|||||||||||||||||||||||||||||||   ||||||   |||||||||
Db        301 TTTGAATCTAAGGTTGCTGATTTTGGACTTGCTAAGTTCACCAGTGATAATAACACTCAT 360

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        361 GTTTCGACAAGAGTAATGGGCACTTTTGGATATCTAGCACCAGAGTACGCATCTTCTGGC 420

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              ||||||||||||||||||||||||||:::|||||||:::||||||||||||||||||||
Db        421 AAGCTCACTGAGAAATCAGATGTCTTCTCCTATGGAGTTATGCTTCTTGAGTTAATAACT 480

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||||||||   :::      |||:::||||||||||||||||||||||||
Db        481 GGTCGTCGGCCAGTTGATACAAGTCAAACATATATGGATGACAGCTTGGTTGACTGGGCA 540

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
              ||||||||||||   :::|||   |||   |||::::::|||   |||   |||   :::
Db        541 AGGCCTTTACTGATGCAAGCACTTGAGAATGGTAACTACGAGGAGTTAGTAGATCCTCGG 600

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
              :::       ::::::      ||||||||||||||:::||||||||||||||||||
Db        601 CTTGGGAAGGATTTCAATCCCAATGAGATGGCGAGAATGATTGCTTGTGCAGCTGCATGC 660

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGly 550
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        661 GTACGCCATTCCGCTCGTCGTCGCCCACGCATGAGCCAGGTTGTCCGGGCTTTGGAAGGT 720

Qy        551 AsnValSer 553
              :::||||||
Db        721 GACGTGTCT 729

RESULT 9
BG441204
LOCUS       BG441204                692 bp    mRNA    linear   EST 15-MAR-2001
DEFINITION  GA__Ea0012C15f Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0012C15f, mRNA sequence.
ACCESSION   BG441204
VERSION     BG441204.1  GI:13350856
KEYWORDS    EST.
SOURCE      Gossypium arboreum
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 692)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
            Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
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          of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .692
                     /organism="Gossypium arboreum"
                     /mol_type="mRNA"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0012C15f"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
                     /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:
Pred. No.:              9.38e-25        Length:         692
Score:                  1047.00         Matches:        198
Percent Similarity:     94.71%          Conservative:   17
Best Local Similarity:  87.22%          Mismatches:     12
Query Match:            30.32%          Indels:         0
DB:                     12              Gaps:           0

US-10-086-464-2 (1-647) x BG441204 (1-692)

Qy        247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
              ||||||||| |||||||||:::  ||||||||||||||||||||||:::||||||
Db         11 CTTCCGCCTGCGTCACCTGGTATTTCCTTAGGTTTCTCGAAAAGCACTTTTAGCTATGAA 70

Qy        267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
              ||||||||||||||||:::||||||||||||  ||||||||||||||||||||||||
Db         71 GAATTAGCGAGAGCAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT 130

Qy        287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
              ||||||||||||||||||||||||||:::||||||||||||||||||||||||||||||
Db        131 GGGTACGTACACAAAGGAGTTCTCCCTAATGGGAAGGAAGTAGCAGTAAAGCAACTCAAG 190

Qy        307 ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgVal 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTGGAAGTGGGCAAGGCGAGAGAGAATTTCAGGCTGAAGTTGAGATCATTAGCCGCGTC 250

Qy        327 HisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeu 346
              ||||||:::|||||||||||||||||||||||||||||:::|||      |||:::|||
Db        251 CATCACAAACATCTCGTCTCATTGGTCGGATACTGTATTTCTGGGACAATAAGAATGCTT 310

Qy        347 ValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgPro 366
              |||||||||||||||||||||||   ||||||   |||||||||||:::||||||
Db        311 GTTTATGAGTTTGTTCCAAACAACACCTTGGAGTTTCACTTGCATGGGAAGGGGCGACTG 370

Qy        367 ThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyr 386
              ||||||:::|||   ||||||:::||||||||||||||||||||||||:::|||
Db        371 ACCATGGATTGGCCGACAAGGATGAAAATTGCTTTAGGATCTGCAAAAGGACTGGCATAT 430

Qy        387 LeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 406
              ||||||||||||||:::|||||||||||||||||||||||||||:::|||||||||
Db        431 CTTCATGAAGATTGTCATCCTAAGATCATTCACCGTGATATTAAGGCCGCTAATATTCTG 490

Qy        407 IleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAsp 426
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TTGGATTTCAAGTTTGAAGCAAAGGTTGCTGATTTTGGACTAGCGAAAATTGCTTCCGAT 550

Qy        427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyr 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTCAACACGCACGTCTCCACCAGGGTGATGGGTACTTTCGGGTATTTAGCCCCTGAGTAT 610

Qy        447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeu 466
              |||:::|||||||||||||||:::||||||||||||||||||||||||:::||||||
Db        611 GCTTCAAGTGGAAAGCTCACTGATAAATCAGATGTTTTCTCCTTCGGGGTCATGCTTTTG 670

Qy        467 GluLeuIleThrGlyArgArg 473
              |||||||||||||||   |||
Db        671 GAGTTGATTACCGGTCACAGA 691

RESULT 10
CD839231
LOCUS       CD839231                723 bp    mRNA    linear   EST 10-JUL-2003
DEFINITION  RFO2.114I04F010529 RFO2 Brassica napus cDNA clone RFO2114I04, mRNA
            sequence.
ACCESSION   CD839231
VERSION     CD839231.1  GI:32521171
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .723
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="samourai (restored line)"
                     /db_xref="taxon:3708"
                     /clone="RFO2114I04"
                     /tissue_type="anthers"
                     /clone_lib="RFO2"
ORIGIN

Alignment Scores:
Pred. No.:              3.37e-24        Length:         723
Score:                  1030.00         Matches:        199
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.83%          Indels:         0
DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x CD839231 (1-723)

Qy        449 SerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeu 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTGCTTTTGGAGCTC 61

Qy        469 IleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAsp 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATTACCGGGCGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTTGAC 121

Qy        489 TrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGAGGGTTTAGCTGAT 181

Qy        509 AlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAla 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GCAAAGATGAATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGTGCTGCG 241
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Qy        529 AlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeu 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATTGTGCGTGCGTTA 301

Qy        549 GluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnVal 568
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GAAGGAAATGTATCACTGTCAGATCTTAACGAAGGGATGAGACCAGGTCAAAGCAATGTA 361

Qy        569 TyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLys 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAG 421

Qy        589 LysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsn 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 AAGTTTAGGAAAATGGCTCTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAAT 481

Qy        609 ProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg 628
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 CCGACCAGCGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 541

Qy        629 GluMetGluMetGlyLysIleLysArgThrGlyGlnGlyTyrSerGlyProSerLeu 647
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCTT 598
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RESULT 11
AY108241
LOCUS AY108241 1053 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO134818 mRNA sequence.
ACCESSION AY108241
VERSION AY108241.1 GI:21211319
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1053)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1053)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES Location/Qualifiers
source 1. .1053
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:637889"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
ORIGIN

Alignment Scores:
Pred. No.: 5.61e-24 Length: 1053
Score: 1027.50 Matches: 203
Percent Similarity: 79.93% Conservative: 28
Best Local Similarity: 70.24% Mismatches: 46
Query Match: 29.76% Indels: 12
DB: 11 Gaps: 4

US-10-086-464-2 (1-647) x AY108241 (1-1053)

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Qy        365 ArgProThrMetGluTrpSerThrArgLeuLysIle-AlaLeuGlySerAlaLysGlyLe 384
              ||||||      ||||||      ||||||||||||     |||||||:||||||||||||
Db          6 CGTCCG------GAGTGGCCTGCTAGATTAAAGATCATGTTTGGGTGCTGCCAAGGGTTT 59

Qy        384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404
              |:::||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db         60 AGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCATCTAA 119

Qy        404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424
              |||||||:::||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        120 CATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGATTTTGGACTTGCAAAGTTCAC 179

Qy        424 aSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaPr 444
              :::|||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTGGCACC 239

Qy        444 oGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVa 464
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||::
Db        240 TGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGAGTCAT 299

Qy        464 lLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAs 484
              :||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        300 GCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATGGATGA 359

Qy        484 pSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGl 504
              ||||||||||||||||||||||||||||||    ||||||    |||    ||::::::::
Db        360 CAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAATATGA 419

Qy        504 uGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetVa 524
              :  |||   |||   ::::::          ::::::          ||||||||||||||::
Db        420 TGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGAATGAT 479

Qy        524 lAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||::
Db        480 AGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGTCAGGT 539

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564
              :|||||||||||||||||||||||||||||    ||||||||||||||:::|||||||||
Db        540 CGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGGCCTGG 599

Qy        564 yGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAs 584
              |   |||      :::   ||||||     |||:::|||||||||||   |||||||||
Db        600 CCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAGTACAA 656

Qy        584 nGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGl 604
              ||||||||||||||||||:::|||||||||                          :::
Db        657 CGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACCAGCAG 710

Qy        604 yGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSerGluGl 624
              :::||||||   ||||||||||:::||||||     ||||||   ||||||||||||||||
Db        711 CCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGCGAGGG 770

Qy        624 yGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly-------------- 639
              |      |||:::|||||||||   |||   :::|||:::   |||
Db        771 CCACCAGACGCAAGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGTGGCTA 830

Qy        640 ----GlnGlyTyrSerGlyProSer 646
                  ||||||||||||   |||
Db        831 CAGCTCAGGATACAGCGGAGCCTCG 855
```

RESULT 12
AY108243
LOCUS AY108243 1016 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays PCO134814 mRNA sequence.
ACCESSION AY108243
VERSION AY108243.1 GI:21211321

```
KEYWORDS    HTC.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1016)
  AUTHORS   Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
            Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
  TITLE     Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
  JOURNAL   Unpublished (2002)
REFERENCE   2  (bases 1 to 1016)
  AUTHORS   Coe,E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source          1. .1016
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:637888"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Cornsensus
                     Library"
                     /note="this sequence is part of a project of EST
                     assemblies resulting from the application of public
                     contigs to seed DuPont contigs; this resource was
                     assembled by DuPont as part of a collaboration for the
                     overgo addressing of BACs in conjunction with the Maize
                     Mapping Project"
ORIGIN

Alignment Scores:
Pred. No.:              6.53e-24        Length:         1016
Score:                  1025.00         Matches:        200
Percent Similarity:     82.14%          Conservative:   30
Best Local Similarity:  71.43%          Mismatches:     42
Query Match:            29.68%          Indels:         8
DB:                     11              Gaps:           4

US-10-086-464-2 (1-647) x AY108243 (1-1016)

Qy        373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
              ||||||||||||||||||||:::|||||||||||||:::|||||||||||||||||||:::
Db          3 AGATTAAAGATCGCTCTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCAT 62

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db         63 CCAAAGATCATCCACCGCGACATTAAGGCATCTAACATTCTTCTTGACTTCAAATTTGAA 122

Qy        413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
              |||   ||||||||||||||||||||||||      :::|||   ||||||||||||||||
Db        123 GCTATGGTTGCTGACTTTGGACTTGCAAAGTTCACTACTGATAACAACACCCATGTGTCA 182

Qy        433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACAAGAGTAATGGGCACCTTTGGGTATTTGGCACCCGAGTATGCAGCATCTGGCAAGCTC 242

Qy        453 ThrGluLysSerAspValPheSerPheGlyValValLeuGluLeuIleThrGlyArg 472
              ||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        243 ACAGAAAAATCCGATGTATTTTCTTTCGGAGTCATGCTTCTTGAGCTTATTACTGGGCGG 302

Qy        473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
              ||||||:::|||            |||:::|||||||||||||||||||||||||||||
Db        303 CGACCAATTGACACAACCCAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGGCCA 362

Qy        493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
              ||||||   ||||||   |||   |||:::::::::   |||   |||   ::::::
Db        363 TTACTGATGAGAGCGCTCGAGGATGGTGAATATGATGCTTTGGTGGATCCTCGGCTCGGA 422

Qy        513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
                  ::::::     |||||||||||||||:::|||||||||||||||||||||||||
Db        423 AAGGACTTCAATCCTAACGAGATGGCAAGAATGATAGCCTGTGCGGCTGCGTGCGTACGC 482

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552
              ||||||||||||||||||||||||||||||:::|||||||||||||||||:::|||
Db        483 CATTCCGCACGTCGTCGGCCACGAATGAGTCAGGTCGTTCGGGCTCTGGAAGGCGACGTG 542

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572
              ||||||   ||||||||||||||:::|||||||||   |||       :::   ||||||
Db        543 TCTTTGGAGGACCTTAATGAAGGTGTTCGACCTGGCCATAGCCGCTTCTTTGGGTCATAT 602

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592
                  |||:::|||||||||||   ||||||||||||||||||:::||||||||||||
Db        603 ---AGCAGCTCTGATTACGATTCCGGGCAGTACAACGAGGACATGCAGAAGTTCAGGAAG 659

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612
                  |||                 |||   ::::::   :::||||||   |||||||||:::
Db        660 ACGGCGTTCAATAACAACACCTACACCAGCAGC---CAATACAGCGCGCCAACCAGTGAA 716

Qy        613 TyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMet---Glu 631
              ||||||      ||||||||||||||||||||||:::   |||:::||||||   |||
Db        717 TACGGCCAGGTGCCGTCTGGATCAAGCAGCGAGGGCCGCCAGACGCAGGAGATGGAGGAG 776

Qy        632 MetGlyLysIleLysArgThrGly--------------GlnGlyTyrSerGlyProSer 646
                  |||   :::|||:::   |||                 ||||||||||||   |||
Db        777 TCGGGTGCAGTGAAGAAAGGTGGCTACAGCGGCTACAGCTCCGGATACAGCGGAGCCTCG 836

RESULT 13
BM358715
LOCUS       BM358715                 666 bp    mRNA    linear   EST 09-JAN-2002
DEFINITION  GA__Ea0012D16r Gossypium arboreum 7-10 dpa fiber library Gossypium
            arboreum cDNA clone GA__Ea0012D16r, mRNA sequence.
ACCESSION   BM358715
VERSION     BM358715.1  GI:18099461
KEYWORDS    EST.
SOURCE      Gossypium arboreum
  ORGANISM  Gossypium arboreum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
            Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
  TITLE     An integrated analysis of the genetics, development, and evolution
            of the cotton fiber
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total High Quality bases = 646
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 666.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Gossypium arboreum"
                     /mol_type="mRNA"
                     /strain="AKA"
                     /cultivar="8400"
                     /db_xref="taxon:29729"
                     /clone="GA__Ea0012D16r"
                     /tissue_type="Fibers isolated from bolls harvested 7-10
                     dpa"
                     /lab_host="E. coli"
```

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
ORIGIN

Alignment Scores:

Pred. No.:	7.55e-24	Length:	666
Score:	1018.00	Matches:	191
Percent Similarity:	95.41%	Conservative:	17
Best Local Similarity:	87.61%	Mismatches:	10
Query Match:	29.48%	Indels:	0
DB:	12	Gaps:	0

US-10-086-464-2 (1-647) x BM358715 (1-666)

```
Qy        247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
              ||||||||||||||||||||:::   ||||||||||||||||||||||||:::||||||
Db         11 CTTCCGCCTCCGTCACCTGGTATTTCCTTAGGTTTCTCGAAAAGCACTTTTAGCTATGAA 70

Qy        267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
              ||||||||||||||||||:::||||||||||   ||||||||||||||||||||||||||
Db         71 GAATTAGCGAGAGCAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT 130

Qy        287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        131 GGGTACGTACACAAAGGAGTTCTCCCTAATGGGAAGGAAGTAGCAGTAAAGCAACTCAAG 190

Qy        307 ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgVal 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GCTGGAAGTGGGCAAGGCGAGAGAGAATTTCAGGCTGAAGTTGAGATCATTAGCCGCGTC 250

Qy        327 HisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeu 346
              ||||||:::||||||||||||||||||||||||||||:::|||      |||:::|||
Db        251 CATCACAAACATCTCGTCTCATTGGTCGGATACTGTATTTCTGGGACAATAAGAATGCTT 310

Qy        347 ValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgPro 366
              ||||||||||||||||||||||   ||||||   ||||||||||:::||||||
Db        311 GTTTATGAGTTTGTTCCAAACAACACCTTGGAGTTTCACTTGCATGGGAAGGGGCGACTG 370

Qy        367 ThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyr 386
              ||||||:::|||   ||||||:::||||||||||||||||||||||||||:::|||
Db        371 ACCATGGATTGGCCGACAAGGATGAAAATTGCTTTAGGATCTGCAAAAGGACTGGCATAT 430

Qy        387 LeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeu 406
              ||||||||||||||:::||||||||||||||||||||||||||:::|||||||||
Db        431 CTTCATGAAGATTGTCATCCTAAGATCATTCACCGTGATATTAAGGCCGCTAATATTCTG 490

Qy        407 IleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAsp 426
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 TTGGATTTCAAGTTTGAAGCAAAGGTTGCTGATTTTGGACTAGCGAAAATTGCTTCCGAT 550

Qy        427 ThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyr 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GTCAACACGCACGTCTCCACCAGGGTGATGGGTACTTTCGGGTATTTAGCCCCTGAGTAT 610

Qy        447 AlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValVal 464
              |||:::||||||||||||:::||||||||||||||||||||:::
Db        611 GCTTCAAGTGGAAAGCTCACTGATAAATCAGATGTTTTCTCCTTCGGGGTCATG 664

RESULT 14
CA072174
LOCUS       CA072174                695 bp    mRNA    linear   EST 23-SEP-2003
DEFINITION  SCCCAM1004A11.g AM1 Saccharum officinarum cDNA clone SCCCAM1004A11
            5', mRNA sequence.
ACCESSION   CA072174
VERSION     CA072174.1  GI:34924325
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE   1  (bases 1 to 695)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 004  row: A  column: 11
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .695
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCCCAM1004A11"
                     /lab_host="DH10B"
                     /clone_lib="AM1"
                     /note="Organ: Apical meristem and tissues surrounding of
                     mature plants; Vector: pSport1; Site_1: SalI; Site_2:
                     NotI; An unidirectional cDNA library generated from
                     [Apical meristem and  tissues surrounding of mature
                     plants]. cDNA was prepared from polyA+ mRNA  using
                     SuperScript Plasmid System Kit (Invitrogen). The
                     double-strand  cDNAs were fractionated in a sepharose
                     CL-2B 40cm-columns and fragments  sizing between 0.8 and
                     1.5 Kb were directionally cloned into the vector.  Details
                     of each source of RNA and library construction can be
                     obtained at  http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 1.13e-23 | Length: | 695 |
| Score: | 1013.00 | Matches: | 195 |
| Percent Similarity: | 91.85% | Conservative: | 19 |
| Best Local Similarity: | 83.69% | Mismatches: | 16 |
| Query Match: | 29.34% | Indels: | 3 |
| DB: | 13 | Gaps: | 1 |

US-10-086-464-2 (1-647) x CA072174 (1-695)

```
Qy   271 AlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHis 290
              ||||||||||||||||||:::||||||||||||||||||||||||||:::|||||||
Db   4 GCAACCAATGGGTTTTCTGACGCTAATCTGCTGGGGCAAGGCGGTTTTGGGTTTGTTCAC 63

Qy   291 LysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGly 310
              ||||||||||||||:::||| ||||||||||||||||||::: |||||||||
Db   64 AAAGGAGTGCTACCAAATGGCACAGAGGTTGCTGTTAAGCAGTTAAGAGATGGAAGTGGC 123

Qy   311 GlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHis 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db   124 CAGGGAGAACGCGAGTTTCAGGCAGAGGTTGAGATTATCAGCAGAGTACATCACAAGCAT 183

Qy   331 LeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPhe 350
              ||||||||||||||||||||||||||:::||||||| ||||||||||||||||||||
Db   184 CTTGTATCCTTGGTCGGCTATTGCATTTCTGGAGCCAACAGGTTGCTCGTCTACGAGTTT 243

Qy   351 ValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              |||||||||||| |||||| ||||||||||:::|||||||||||||:::|||
Db   244 GTTCCAAACAATACATTGGAATTCCACTTACATGGAAAAGGCAGACCAACCTTGGATTGG 303

Qy   371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db   304 CCGACAAGACTAAAAATTGCTCTGGGTTCTGCGAAGGGATTGGCATATCTTCATGAAGAT 363

Qy   391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::|||||||||||||||||||||||||||||||||||||||||:::||| :::
Db   364 TGCCATCCTAAGATCATTCATCGTGACATAAAGGCCTCAAATATTCTTCTTGATCTAAGA 423
```
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```
Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db        424 TTTGAAGCTAAGGTGGCAGATTTTGGACTTGCAAAATTCACTTCTGATACAAACACCCAT 483

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GTTTCAACCAGAGTAATGGGCACATTTGGGTACCTAGCACCTGAGTATGCTGCTTCTGGC 543

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        544 AAGCTCACTGAGAAATCAGATGTCTTCTCTTTTGGAGTAATGCTTCTTGAGCTAATAACT 603

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
              ||||||||||||        |||:::        ||||||:::|||   |||||||||
Db        604 GGGCGGCGTCCT------GGTAATTCAAGACAGGCAGATGACAACTTGGGTGACTGGGCA 657

Qy        491 Arg-ProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
              ||| ||||||:::|||:::|||   |||   |||:::
Db        658 AGGGCCTTTGATGAATAAAGCATTTGAGGATGGTAAT 694

RESULT 15
BU099573
LOCUS       BU099573                715 bp    mRNA    linear   EST 29-AUG-2002
DEFINITION  WHE3309_A09_A17ZS Chinese Spring wheat drought stressed root cDNA
            library Triticum aestivum cDNA clone WHE3309_A09_A17, mRNA
            sequence.
ACCESSION   BU099573
VERSION     BU099573.1  GI:22547372
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 715)
  AUTHORS   Anderson,O.D., Chao,S., Close,T.J., Crossman,C., Fenton,R.D.,
            Lazo,G.R., Nguyen H.T., Pham,J., Rausch,C.J., Turuspekov,Y.,
            Wilson,C., Woo,J. and Zhang,D.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Chinese Spring drought stressed root cDNA library
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequences have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: SK primer.
FEATURES             Location/Qualifiers
     source          1. .715
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE3309_A09_A17"
                     /tissue_type="root"
                     /dev_stage="Full tillering stage"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Chinese Spring wheat drought stressed root
                     cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown under
                     normal conditions, then drought stressed to 80%, 70% and
                     60% RWC at Texas Tech University (D. Zhang in HT Nguyen
                     lab). Total RNA was prepared separately for roots
                     collected at the three different drought conditions. Equal
                     amounts of total RNA were pooled from all three samples,
                     poly(A) RNA were purified, one cDNA library was made, and
                     the cDNA clones were in vivo excised to give pBluescript
                     SK(-) phagemids in the TJ Close lab at the University of
                     California, Riverside (Fenton, Turuspekov). Plasmid DNA
                     preparations and DNA sequencing were performed in the OD
                     Anderson lab (all other authors)."
ORIGIN

Alignment Scores:
Pred. No.:              1.04e-22        Length:         715
Score:                  983.00          Matches:        184
Percent Similarity:     89.70%          Conservative:   25
Best Local Similarity:  78.97%          Mismatches:     24
Query Match:            28.47%          Indels:         0
DB:                     13              Gaps:           0

US-10-086-464-2 (1-647) x BU099573 (1-715)

Qy        276 SerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPro 295
              |||:::|||||||||||||||||||||||||||||:::|||||||||||||||||||
Db         11 TCCGATGCTAATCTTCTCGGGCAAGGTGGCTTTGGATTTGTTCACAAAGGAGTGCTGCCA 70

Qy        296 SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGlu 315
              |||   ||||||||||||||||||||||:::   ||||||||||||||||||||||||
Db         71 GATGGCACAGAAGTTGCTGTGAAGCAATTAAGAGATGGAAGTGGGCAGGGAGAGCGTGAG 130

Qy        316 PheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVal 335
              ||||||||||||||||||||||||||||||||||||||:::||||:||||:::||||||
Db        131 TTCCAGGCAGAGGTTGAGATTATCAGCCGAGTACATCATAAACATCTCGTGACATTGGTT 190

Qy        336 GlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsn 355
              ||||||||||||:::      ||||||||||||||||||||||||||||||||||||
Db        191 GGTTATTGCATTTCTGAAGACAAGAGGTTGCTTGTCTATGAGTTTGTTCCCAATAACACG 250

Qy        356 LeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLys 375
              ||||||   |||:::|||||          |||||||||:::|||   :::|||||||:::
Db        251 TTAGAATTCCATATACATGGAAGGCGTGGACCAACTATGGACTGGCCTTCAAGACTACGT 310

Qy        376 IleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIle 395
              ||||||||||||||||||||||||:::|||||||||||||||||:::||||||||||
Db        311 ATTGCTTTGGGTTCTGCGAAGGGATTGGCGTATCTTCACGAAGACTGCCATCCAAAGATC 370

Qy        396 IleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysVal 415
              ||||||||||||||||||||||||||||:::|||::::::   ||||||||||||
Db        371 ATTCATCGTGACATAAAGGCATCAAATATTCTTCTGGATTACAGATGTGAAGCTAAGGTG 430

Qy        416 AlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVal 435
              ||||||||||||||||||:::   ||||||   ||||||||||||||||||||||||
Db        431 GCAGATTTTGGACTTGCAAAGTTAACCTCTGATAATAACACTCATGTTTCCACCAGAGTA 490

Qy        436 MetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLys 455
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        491 ATGGGCACATTTGGGTACCTTGCACCAGAGTATGCTTCTTCTGGCAAGCTAACTGAGAAA 550

Qy        456 SerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVal 475
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        551 TCAGATGTCTTTTCTTTTGGAGTAATGCTTCTCGAGTTAATAACTGGGCGCCGTCCTGTA 610

Qy        476 AspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsn 495
              :::         ::::::||||||||||||||||||||||||||||||||||:::
Db        611 AGTTCAAAACAAGCGCATATGGATGACAGCTTGGTTGACTGGGCAAGGCCTTTGATGACA 670

Qy        496 ArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAsp 508
              :::|||   |||   |||:::   :::   |||   |||
Db        671 CAAGCACTCGAGGATGGTAATCACGATGCTTTAGTGGAT 709


Search completed: May 13, 2004, 01:33:29
Job time : 3622 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 12, 2004, 22:28:46 ; Search time 139 Seconds
(without alignments)
2583.117 Million cell updates/sec

Title: US-10-086-464-2
Perfect score: 3453
Sequence: 1 MSSAPSPGTGSPPSPPSNST.....REMEMGKIKRTGQGYSGPSL 647

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10086464/runat_11052004_121815_7866/app_query.fasta_1.839
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10086464_@CGN_1_1_85_@runat_11052004_121815_7866 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	756	21.9	3239	4	US-09-228-986-9	Sequence 9, Appli
2	744.5	21.6	1593	4	US-09-602-472A-1	Sequence 1, Appli
3	740	21.4	2868	4	US-09-228-986-4	Sequence 4, Appli
4	712	20.6	1488	4	US-09-579-182-4	Sequence 4, Appli
5	703.5	20.4	2513	4	US-09-228-986-13	Sequence 13, Appl
6	678	19.6	2432	4	US-09-228-986-7	Sequence 7, Appli
7	667.5	19.3	1559	4	US-09-602-472A-3	Sequence 3, Appli
8	604.5	17.5	4104	3	US-08-881-706-1	Sequence 1, Appli
9	602	17.4	1224	4	US-09-579-182-3	Sequence 3, Appli
10	600.5	17.4	3097	4	US-09-228-986-11	Sequence 11, Appl
11	581.5	16.8	3590	1	US-08-587-889-1	Sequence 1, Appli
12	581.5	16.8	3590	4	US-09-016-434-1093	Sequence 1093, Ap
13	581.5	16.8	3590	5	PCT-US96-09193-1	Sequence 1, Appli
14	578	16.7	2114	4	US-09-602-472A-5	Sequence 5, Appli
15	575	16.7	2749	1	US-08-265-628-1	Sequence 1, Appli
16	572	16.6	2571	1	US-07-717-331F-9	Sequence 9, Appli
17	572	16.6	2833	1	US-07-717-331F-1	Sequence 1, Appli
18	567	16.4	1554	2	US-08-587-680A-24	Sequence 24, Appl
19	566.5	16.4	2389	4	US-09-228-986-1	Sequence 1, Appli
20	562	16.3	2336	4	US-09-228-986-10	Sequence 10, Appl
21	559.5	16.2	2638	4	US-09-228-986-8	Sequence 8, Appli
22	546	15.8	2749	1	US-07-717-331F-4	Sequence 4, Appli
23	545	15.8	966	1	US-08-447-185-2	Sequence 2, Appli
24	545	15.8	2443	1	US-08-447-185-3	Sequence 3, Appli
25	543	15.7	2686	4	US-09-228-986-3	Sequence 3, Appli
26	531.5	15.4	5733	2	US-08-473-553A-1	Sequence 1, Appli
27	486	14.1	2943	4	US-09-503-922-2	Sequence 2, Appli
28	460.5	13.3	2649	4	US-09-228-986-12	Sequence 12, Appl
29	430	12.5	2568	4	US-09-228-986-2	Sequence 2, Appli
c 30	401	11.6	1926	4	US-09-249-585A-2	Sequence 2, Appli
c 31	401	11.6	1926	4	US-09-410-399-3	Sequence 3, Appli
c 32	401	11.6	2580	3	US-09-050-863-2	Sequence 2, Appli
c 33	401	11.6	2580	4	US-09-359-081-2	Sequence 2, Appli
34	401	11.6	5452	2	US-09-130-114-1	Sequence 1, Appli
35	401	11.6	8705	4	US-09-647-344A-14	Sequence 14, Appl
c 36	401	11.6	9600	3	US-08-910-647-1	Sequence 1, Appli
c 37	401	11.6	9600	4	US-09-620-925-1	Sequence 1, Appli
c 38	401	11.6	10596	1	US-07-884-811-15	Sequence 15, Appl
c 39	401	11.6	10596	1	US-07-885-971-15	Sequence 15, Appl
c 40	401	11.6	10596	1	US-08-087-783A-15	Sequence 15, Appl
c 41	401	11.6	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 42	401	11.6	10596	2	US-08-194-087-15	Sequence 15, Appl
c 43	401	11.6	10596	5	PCT-US93-04648-15	Sequence 15, Appl
44	401	11.6	16080	4	US-09-724-566A-48	Sequence 48, Appl
45	395.5	11.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-228-986-9
; Sequence 9, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 3239
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-228-986-9

Alignment Scores:
Pred. No.: 1.88e-23 Length: 3239
Score: 756.00 Matches: 190
Percent Similarity: 51.93% Conservative: 92
Best Local Similarity: 34.99% Mismatches: 132
Query Match: 21.89% Indels: 130
DB: 4 Gaps: 17

US-10-086-464-2 (1-647) x US-09-228-986-9 (1-3239)

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Qy          89 ProProAlaProVal-ThrProProThrArgAsnProProProSerValProGlyProPr 108
               ||||||   |||       |||   |||   :::|||||||||   :::         ||
Db        1759 CCTCCCAAACCATTCGGCCCCTATTACTTCATCGCCTCCCCCTATGCTTTT-------CC 1811

Qy         108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
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Db       1812 AGACAAT-----------GGAGGAACC------------------------------ 1827

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148

Db       1828 ------------GCCATAAGCAAAGGTGTGATAGTTGGGATCGCTATTGGCGGCACGGT 1874

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db       1875 TCTGGTTCTTGGCCTTGTTGTATTAGGGTTATATGCTATTCGACAAAAGAAACGGGCGGA 1934

Qy        168 uGluAspAlaTyrTyrValProProPro-----------ProProProGlyProLysAl 184

Db       1935 GAAA---GCTCTCGAGTTGAGCAGACCCTTCGCATCCTGGGCACCCAGTGGGAAAGATAG 1991

Qy        184 aGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSe 204

Db       1992 CGGAGGAGCGCCACAACTGAAAGGAGCACGATGG------------------------- 2025

Qy        204 rAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGlnPr 224

Db       2025 ------------------------------------------------------------ 2025

Qy        224 oProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAspAr 244

Db       2025 ------------------------------------------------------------ 2025

Qy        244 gProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheTh 264

Db       2026 ----------------------------------------------------------TTCTC 2030

Qy        264 rTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGl 284

Db       2031 CTATGATGAACTTAAGAGGTGCACCAATAATTTCTCCGATAGCAATGAATTAGGCTTCGG 2090

Qy        284 yGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGl 304

Db       2091 AGGATACGGAAAGGTGTACAGGGGAGTTCTTCCTGATGGTCATATATTAGCAATCAAAAG 2150

Qy        304 nLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSe 324

Db       2151 AGCTCAGCAGGGGTCGATGCAGGGTGCAACCGAGTTCAAGACAGAAATCGAGCTGCTTTC 2210

Qy        324 rArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysAr 344

Db       2211 GCGGGTTCATCACAAGAATCTTGTTGGCCTCATAGGATTCTGTTTCGAGCAAGGAGAGCA 2270

Qy        344 gLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGl 364

Db       2271 GATGTTGGTCTATGAATATATGCCTAACGGGACGCTCAGGGATAGCTTGACAGGAAAATC 2330

Qy        364 yArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLe 384

Db       2331 AGGCATTTATCTTGATTGGAAGAGGAGGCTTCGTATAGCTCTAGGTTCGGCTAGAGGACT 2390

Qy        384 uSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSerAs 404

Db       2391 AGCTTATCTGCACGAACTCGCGAATCCTCCAATTATCCACAGAGATGTCAAGTCCACCAA 2450

Qy        404 nIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAl 424

Db       2451 TATCTTGTTGGACGAACATCTGACGGCCAAAGTCGCGGATTTCGGTTTGTCCAAACTGGT 2510

Qy        424 aSerAspThrAsnThr---HisValSerThrArgValMetGlyThrPheGlyTyrLeuAl 443

Db       2511 ATCGGACAGCGGGAAGGGGCACGTTTCGACGCAAGTGAAAGGCACGCTGGGCTATTTGGA 2570

Qy        443 aProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVa 463

Db       2571 TCCCGAATACTACATGAGTCAACAGCTGACAGAAAAGAGCGATGTGTACAGCTTCGGGGT 2630

Qy        463 lValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAs 483

Db       2631 GGTCATGCTTGAGCTCATCACTGCAAAGCAACCGATTGAGAAGGGCAAGTATGTCGTCCG 2690

Qy        483 pAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPh 503

Db       2691 CGAG--------------ATTCGCACCGCCATGGACAAGAACGACCAG------GACTA 2729

Qy        503 eGluGly---------LeuAlaAspAlaLysMetAsnAsn---GlyTyrAspArgGluGl 519

Db       2730 CTACGGCGTGAGGGAAATGATGGACCCGTCCATGAGGAGCATGGGCTAC---CTCGTCGG 2786

Qy        519 uMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPr 539

Db       2787 GTTCAGCAGGTTCTTGGATTTGGCGATGCGATGTGTCGAGGAGTCGGCTGCGGACCGCCC 2846

Qy        539 oArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGl 559

Db       2847 CACAATGAGCGAGGTGGTGAAGGCGATCGAGACCATGTTGCAG------------AACGA 2894

Qy        559 uGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAs 579

Db       2895 TGGGATACACACCAACTCGACGTCCGCATCGTCGTCG---------GCGACGGACTTTGG 2945

Qy        579 pSerSerGln-----------------TyrAsnGluAspMetLysLysPheArgLysMe 593

Db       2946 GTCGACGAAGGGCGCTCCTCGGCATCCGTACAACGATGCCTTACCCAAG----------- 2994

Qy        593 tAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTy 613

Db       2995 -------AAGGAAGTTAGCTATAGCGATTCCTTTGATTATAGT---------GGTGGATA 3038

Qy        613 rGlyLeu 615

Db       3039 TGGACTA 3045
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RESULT 2
US-09-602-472A-1
; Sequence 1, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1593
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
US-09-602-472A-1

Alignment Scores:

Pred. No.:	2.9e-23	Length:	1593
Score:	744.50	Matches:	172
Percent Similarity:	57.07%	Conservative:	66
Best Local Similarity:	41.25%	Mismatches:	116
Query Match:	21.56%	Indels:	63
DB:	4	Gaps:	9

US-10-086-464-2 (1-647) x US-09-602-472A-1 (1-1593)

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Qy        235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeu 254

Db        181 TCGTCGGGTTCGAAAGACGGGTCGCAGGGTCAGATT---------------------- 216

Qy        255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274

Db        217 ------------GCTGCTCATACATTCACTTTCCGGGAGCTTGCAGCTGCAACAAACAAT 264
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Qy        275 PheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294
Db        265 TTTAGCCCTGATTGTTTGCTAGGAGAAGGAGGGTTTGGCCATGTGTATAGAGGACGGCTT 324

Qy        295 Pro---SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGlu 313
Db        325 CCGGGCAGCGGTCAGATTGTAGCTGTCAAACAATTGGATAGGAACGGGCTGCAGGGTAAC 384

Qy        314 ArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSer 333
Db        385 CGTGAATTTCTCGTAGAAGTTCTTATGCTCAGCCTTTTACATCATCCCAATTTGGTGAAT 444

Qy        334 LeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsn 353
Db        445 TTAATCGGATACTGTGCTGATGGTGACCAAAGACTTCTTGTTTATGAATTCATGCCATTG 504

Qy        354 AsnAsnLeuGluLeuHisLeuHisGly------GluGlyArgProThrMetGluTrpSer 371
Db        505 GGATCGTTAGAAGATCATCTTCATGATCTCCCACCAGAAAAAGAAGCGTTAGATTGGAAC 564

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391
Db        565 ACAAGAATGAAGATAGCGGCTGGTGCAGCTCGAGGTTTGGAATTTCTTCACGATAAGGCT 624

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411
Db        625 AATCCTCCTGTTATTTACAGGGATTTCAAATCATCAAACATTTTGCTCGGTGAGGGATTT 684

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAla---SerAspThrAsnThrHis 430
Db        685 CAACCAAAGCTTTCTGATTTCGGGCTAGCGAAGTTGGGCCCGACGGGAGATAAGTCTCAT 744

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
Db        745 GTATCCACACGGGTCATGGGAACGTATGGTTACTGTGCTCCTGAGTATGCGATGACCGGT 804

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
Db        805 CAACTCACTGTTAAGTCTGATGTGTATAGCTTTGGGGTGGTTTTCTTAGAGCTTATTACA 864

Qy        471 GlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAla 490
Db        865 GGCCGAAAAGCCATTGACAGCAGTGCACCGCAAGGACAGCAGAATCTCGTCACTTGGGCA 924

Qy        491 ArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLys 510
Db        925 CGACCCTTATTCAAC---------GACAGAAGGAAATTTGCAACATTGGCAGACCCCAGG 975

Qy        511 MetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCys 530
Db        976 CTTGAAGGACATTATCCCATGAGGGGTCTGTACCAGGCTCTAGCGGTTGCATCGATGTGC 1035

Qy        531 ValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeu------ 548
Db       1036 ATCCAAGAACAGGCTGCGGCTCGACCGCTTATAGGAGACGTGGTCACTGCCTTATCTTAT 1095

Qy        548 ------------------------------------------------------------ 548
Db       1096 CTTGCGAACCACACCTATGATCCCAATGCGGCCTCTGGTCAAAGCAACCGGTACAACAAC 1155

Qy        549 ---GluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsn 567
Db       1156 GGTGAGAGAACCAGTAGAATTTCAAAGAATGAAGAAGGTGGTGGGTCGGGTCGTAGCAGG 1215

Qy        568 ValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln--------------- 582
Db       1216 ---TGGGGGGATCTAGAAGGTTCCGACAAAGGAGATTCGCCTCGAGAAACTCAAACTCCA 1272

Qy        583 ------TyrAsnGluAspMet---------------------------------------- 587
Db       1273 AGGATGCTGAATCGAGATCTTGATCGAGAACGGGCTGTTGCTGAGGCTAAAATGTGGGTA 1332

Qy        588 LysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGly 604
Db       1333 GAAAAAAGACGACAAAGTGCACAAGGCAGCTTTGATGGGAATGCTAACGGT 1383

RESULT 3
US-09-228-986-4
; Sequence 4, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 2868
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-09-228-986-4

Alignment Scores:
Pred. No.:                7.71e-23        Length:          2868
Score:                    740.00          Matches:         182
Percent Similarity:       50.91%          Conservative:    69
Best Local Similarity:    36.92%          Mismatches:      133
Query Match:              21.43%          Indels:          109
DB:                       4               Gaps:            13

US-10-086-464-2 (1-647) x US-09-228-986-4 (1-2868)

Qy         90 ProAlaProValThrProProThrArgAsnProProProSerValProGlyProPro--- 108
Db        858 CCATGTCCGGGATCTCCTCCTTTTTCTCCTCCTCCTCCGTTTGTACCACCCCCGCCAGTA 917

Qy        109 ------SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerPro 126
Db        918 GCTGGAAGCAATGGAGCAAGGGTGCAGAGCTCTTCC---------------------- 953

Qy        127 ProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGly 146
Db        954 ----------------------AGCACAGGAGCCATTGCTGGGGGAGTAGCTGCAGGT 989

Qy        147 ValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArg 166
Db        990 GCTGCCCTCTTATTT------------------------------------------- 1004

Qy        167 AspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGly 186
Db       1005 ----------------------------------------GCAGCTCCTGCAATTGGGTTC 1025

Qy        187 ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHis 206
Db       1026 GCCTGG----------------TGGCGTCGCAGAAAG---------CCACAGGAGCAC 1058

Qy        207 ValValThrSerLeuProProProProLysAlaProSerProProArgGlnProProPro 226
Db       1058 ------------------------------------------------------------ 1058

Qy        227 ProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProVal 246
Db       1059 ----------------------------------------TTCTTTGATGTACCTGCT 1076

Qy        247 LeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu 266
Db       1077 ------GAGGAGGATCCAGAAGTTCACTTAGGCCAACTTAAG---AGGTTCTCATTACGG 1127

Qy        267 GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPhe 286
Db       1128 GAATTACAGGTTGCAACTGATGGTTTTAGCAATAGAAACATTCTTGGCAGAGGTGGTTTT 1187
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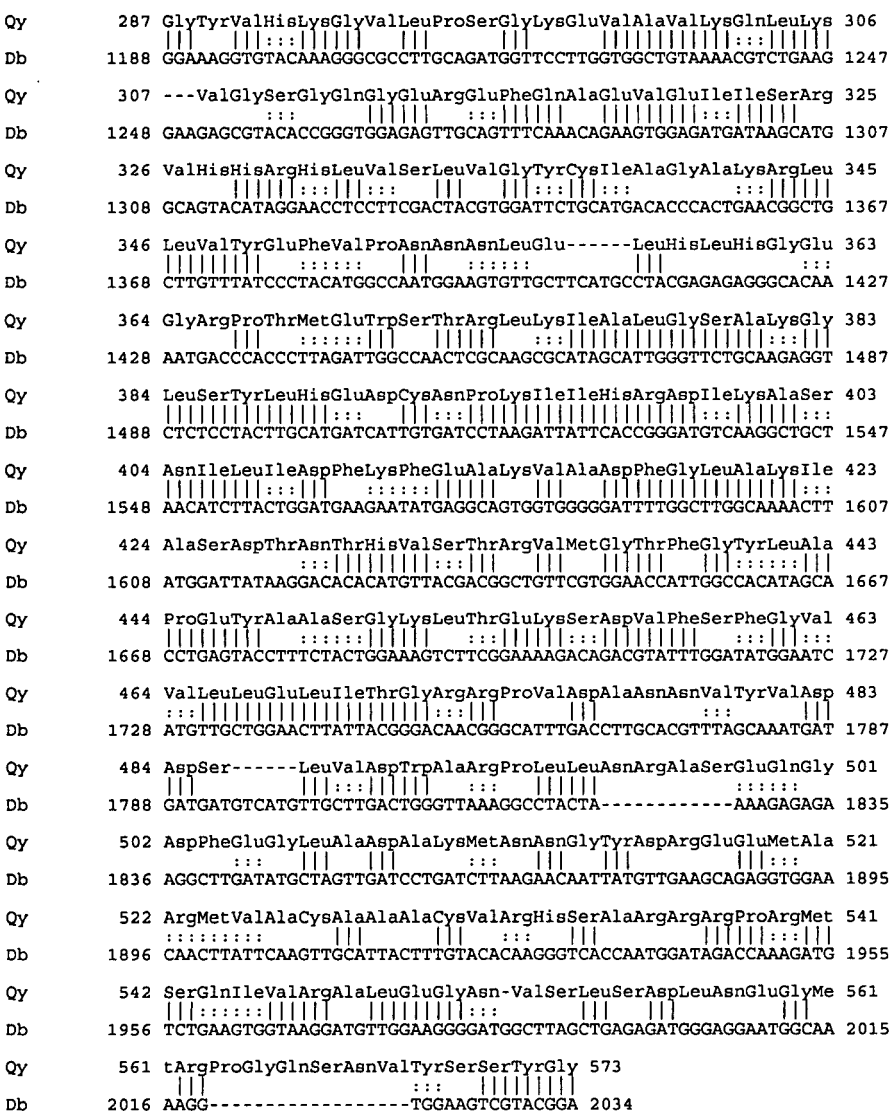

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Qy        287 GlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLys 306
Db       1188 GGAAAGGTGTACAAAGGGCGCCTTGCAGATGGTTCCTTGGTGGCTGTAAAACGTCTGAAG 1247

Qy        307 ---ValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArg 325
Db       1248 GAAGAGCGTACACCGGGTGGAGAGTTGCAGTTTCAAACAGAAGTGGAGATGATAAGCATG 1307

Qy        326 ValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeu 345
Db       1308 GCAGTACATAGGAACCTCCTTCGACTACGTGGATTCTGCATGACACCCACTGAACGGCTG 1367

Qy        346 LeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLeuHisGlyGlu 363
Db       1368 CTTGTTTATCCCTACATGGCCAATGGAAGTGTTGCTTCATGCCTACGAGAGAGGGCACAA 1427

Qy        364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db       1428 AATGACCCACCCTTAGATTGGCCAACTCGCAAGCGCATAGCATTGGGTTCTGCAAGAGGT 1487

Qy        384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
Db       1488 CTCTCCTACTTGCATGATCATTGTGATCCTAAGATTATTCACCGGGATGTCAAGGCTGCT 1547

Qy        404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423
Db       1548 AACATCTTACTGGATGAAGAATATGAGGCAGTGGTGGGGGATTTTGGCTTGGCAAAACTT 1607

Qy        424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443
Db       1608 ATGGATTATAAGGACACACATGTTACGACGGCTGTTCGTGGAACCATTGGCCACATAGCA 1667

Qy        444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463
Db       1668 CCTGAGTACCTTTCTACTGGAAAGTCTTCGGAAAAGACAGACGTATTTGGATATGGAATC 1727

Qy        464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAsp 483
Db       1728 ATGTTGCTGGAACTTATTACGGGACAACGGGCATTTGACCTTGCACGTTTAGCAAATGAT 1787

Qy        484 AspSer------LeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501
Db       1788 GATGATGTCATGTTGCTTGACTGGGTTAAAGGCCTACTA-----------AAAGAGAGA 1835

Qy        502 AspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAla 521
Db       1836 AGGCTTGATATGCTAGTTGATCCTGATCTTAAGAACAATTATGTTGAAGCAGAGGTGGAA 1895

Qy        522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMet 541
Db       1896 CAACTTATTCAAGTTGCATTACTTTGTACACAAGGGTCACCAATGGATAGACCAAAGATG 1955

Qy        542 SerGlnIleValArgAlaLeuGluGlyAsn-ValSerLeuSerAspLeuAsnGluGlyMe 561
Db       1956 TCTGAAGTGGTAAGGATGTTGGAAGGGGATGGCTTAGCTGAGAGATGGGAGGAATGGCAA 2015

Qy        561 tArgProGlyGlnSerAsnValTyrSerSerTyrGly 573
Db       2016 AAGG-----------------TGGAAGTCGTACGGA 2034
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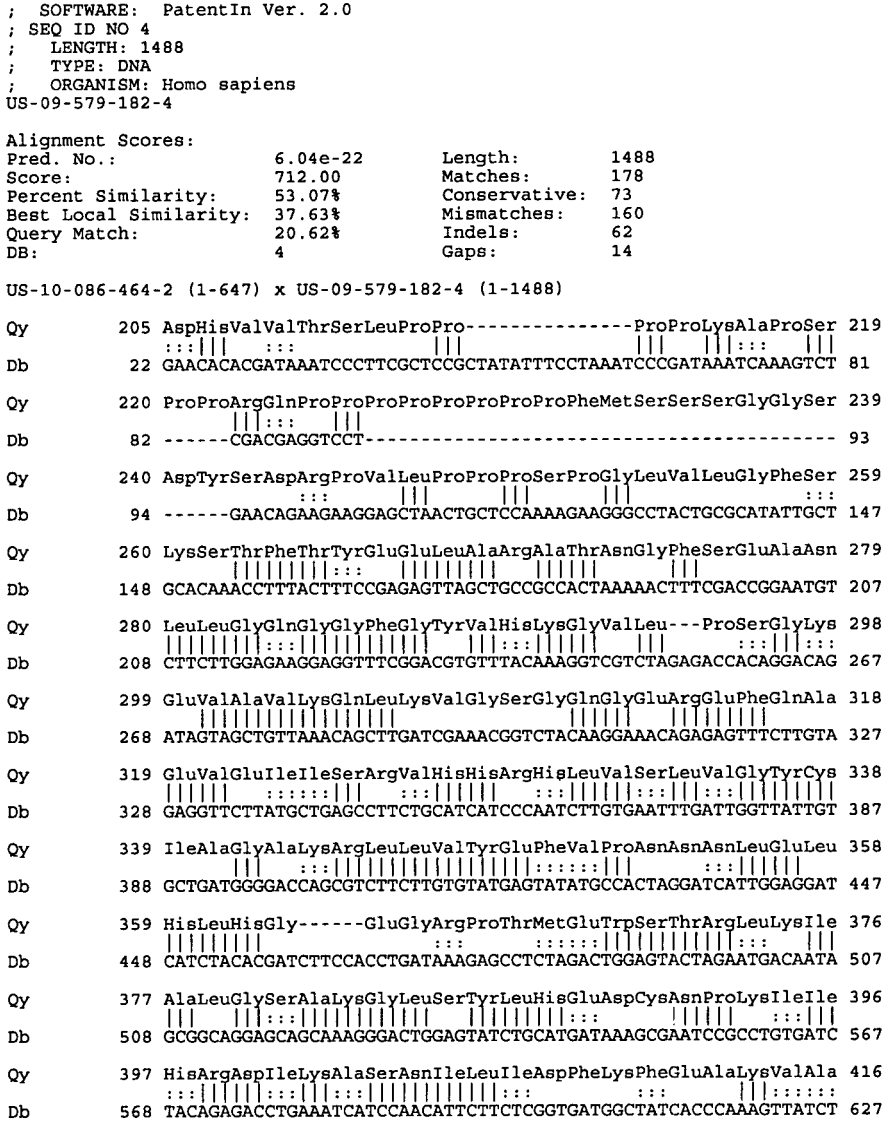
RESULT 4
US-09-579-182-4
; Sequence 4, Application US/09579182
; Patent No. 6500628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-4

Alignment Scores:

Pred. No.:	6.04e-22	Length:	1488
Score:	712.00	Matches:	178
Percent Similarity:	53.07%	Conservative:	73
Best Local Similarity:	37.63%	Mismatches:	160
Query Match:	20.62%	Indels:	62
DB:	4	Gaps:	14

US-10-086-464-2 (1-647) x US-09-579-182-4 (1-1488)



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Qy        205 AspHisValValThrSerLeuProPro--------------ProProLysAlaProSer 219
Db         22 GAACACACGATAAATCCCTTCGCTCCGCTATATTTCCTAAATCCCGATAAATCAAAGTCT 81

Qy        220 ProProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySer 239
Db         82 ------CGACGAGGTCCT---------------------------------------- 93

Qy        240 AspTyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSer 259
Db         94 ------GAACAGAAGAAGGAGCTAACTGCTCCAAAAGAAGGGCCTACTGCGCATATTGCT 147

Qy        260 LysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsn 279
Db        148 GCACAAACCTTTACTTTCCGAGAGTTAGCTGCCGCCACTAAAAACTTTCGACCGGAATGT 207

Qy        280 LeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu---ProSerGlyLys 298
Db        208 CTTCTTGGAGAAGGAGGTTTCGGACGTGTTTACAAAGGTCGTCTAGAGACCACAGGACAG 267

Qy        299 GluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAla 318
Db        268 ATAGTAGCTGTTAAACAGCTTGATCGAAACGGTCTACAAGGAAACAGAGAGTTTCTTGTA 327

Qy        319 GluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCys 338
Db        328 GAGGTTCTTATGCTGAGCCTTCTGCATCATCCCAATCTTGTGAATTTGATTGGTTATTGT 387

Qy        339 IleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeu 358
Db        388 GCTGATGGGGACCAGCGTCTTCTTGTGTATGAGTATATGCCACTAGGATCATTGGAGGAT 447

Qy        359 HisLeuHisGly------GluGlyArgProThrMetGluTrpSerThrArgLeuLysIle 376
Db        448 CATCTACACGATCTTCCACCTGATAAAGAGCCTCTAGACTGGAGTACTAGAATGACAATA 507

Qy        377 AlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIle 396
Db        508 GCGGCAGGAGCAGCAAAGGGACTGGAGTATCTGCATGATAAAGCGAATCCGCCTGTGATC 567

Qy        397 HisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAla 416
Db        568 TACAGAGACCTGAAATCATCCAACATTCTTCTCGGTGATGGCTATCACCCAAAGTTATCT 627

Qy        417 AspPheGlyLeuAlaLysIleAlaSer---AspThrAsnThrHisValSerThrArgVal 435
Db        628 GATTTTGGGTTAGCTAAGTTAGGTCCCGTGGGCGATAAAACACATGTGTCAACTCGTGTG 687

Qy        436 MetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLys 455
Db        688 ATGGGCACATATGGTTATTGTGCACCGGAATATGCCATGACAGGGCAACTCACATTGAAA 747

Qy        456 SerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVal 475
Db        748 TCCGATGTTTATAGCTTTGGGGTTGTGTTTCTCGAGCTCATCACGGGTCGAAAAGCTATT 807
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Qy        476 AspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsn 495
Db        808 GATAATGCTCGAGCACCCGGAGAGCACAACCTTGTCGCATGGGCTAGGCCGTTGTTC--- 864

Qy        496 ArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyr 515
Db        865 ------AAAGATCGTAGAAAGTTTCCGAAGATGGCGGATCCATCGCTGCAAGGGCGGTAT 918

Qy        516 AspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAla 535
Db        919 CCAATGCGTGGTCTATATCAAGCACTTGCAGTTGCAGCAATGTGTTTACAGGAACAAGCA 978

Qy        536 ArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSer 555
Db        979 GCGACAAGACCACTGATTGGCGACGTGGTGACAGCTCTAACATACTTAGCTTCGCAAACG 1038

Qy        556 ---AspLeuAsn------------GluGlyMetArgProGlyGlnSerAsnValTyr--- 569
Db       1039 TTTGACCCAAACGCACCAAGCGGTCAAAACAGTAGAAGTGGGAGTGGGCCACCATTTATC 1098

Qy        570 ------------------SerSerTyrGlyGlySerThrAspTyrAsp------------ 579
Db       1099 AGAACAAGGGATGATCGGAGGAGCTTGGGAGATGGGAGTAGCTTGGATAGTCCTGCAGAG 1158

Qy        580 ------------------SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMet 593
Db       1159 ACTCGGAGTCGGTTAGGGTCACCAGCCACTCACAAGAACTCTCCTGATTACAGAAGAAGG 1218

Qy        594 AlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSer------ 611
Db       1219 GATATG---GTGAGGGAAGTCAATGCAGGATCAGAAGGTGGGAGCGAGACAGGAGGCGGG 1275

Qy        612 ---------AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArg 628
Db       1276 TCAGGTAGAAAATGGGGATTA------------AGCGATTTGGAAGGGCAAGAATCACAG 1323

Qy        629 GluMetGluMetGlyLysIleLysArgThrGlyGlnGly 641
Db       1324 AGAGGGAGCCCGGCGAGTGTTGGGAGATCATCGAGAGGC 1362
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RESULT 5
US-09-228-986-13
; Sequence 13, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2513
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-13

Alignment Scores:

Pred. No.:	2.21e-21	Length:	2513
Score:	703.50	Matches:	178
Percent Similarity:	49.52%	Conservative:	81
Best Local Similarity:	34.03%	Mismatches:	179
Query Match:	20.37%	Indels:	85
DB:	4	Gaps:	14

US-10-086-464-2 (1-647) x US-09-228-986-13 (1-2513)

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Qy         84 ThrThrProGlySerProProAlaProValThrProProThrArgAsnProProProSer 103
Db        795 ACTGGTCCTGCTCCTCCTCCCCCACCATATACTCCACCT---------------------- 833

Qy        104 ValProGlyProProSerAsnProSerArgGluGlyGlySerProArgProProSerSer 123
Db        834 ---------CCACCTTCTAAC--------------------AATCGGCCACCCAAGTCC 863

Qy        124 ProSer------ProProSerProSerSerAspGly--------------------Leu 134
Db        864 TCAAATGTGGTCCCTTCATCAGGTGGCTCAAAGGGTGGGAACAGCAATAAGAAATCTCTG 923

Qy        135 SerThrGlyValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThr 154
Db        924 AGTGGTGGTGCCATAGTGGGTATAATATTTGCAGTTATTTTGACTGTTGTTGCTGCTATA 983

Qy        155 LeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAlaTyrTyrVal 174
Db        984 TTAGGAGTTATTTTATATGCACGTAAGTCTCCTAGAAGAGAGCAGGAT------------ 1031

Qy        175 ProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGln 194
Db       1032 ----------------------------------------------GAAGAAAAACTA 1043

Qy        195 TrpArgGlnGlnAsnAlaThrPro------ProSerAspHisValValThrSerLeuPro 212
Db       1044 AGCAATCGTGTGTCTTTCACCCCCCTATCTCCCCTCGATGCTGAATTATTGAAAGAGAGT 1103

Qy        213 ProProProLysAlaProSerProProArgGlnProProProProProProProProPhe 232
Db       1104 CCAGAGCAAAAAGTCAGCTCATCACCTCTTGAAATCGCTCTTAAGCCTCCCCCTTCTGAA 1163

Qy        233 MetSerSerSerGly--------------GlySerAspTyrSerAspArgProValLeu 247
Db       1164 CGCAACAAGTCTACAGGGGACAAAGGCTTCGGAAGTATTTTTTCAAGTAAGAGGACTAAA 1223

Qy        248 ProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGlu 267
Db       1224 AACCCA----------------------ATATCAGCAACTGAATATTCTATTGCAGAC 1259

Qy        268 LeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGly 287
Db       1260 CTGCAAATGGCAACAAATAGTTTTAGTCAAGATAATCTTATTGCGGAGGGTGCTCTTGGA 1319

Qy        288 TyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysVal 307
Db       1320 CGAATCTACCGAGCAGAGTTTCCAGATGGAAAGATTTTGGCAGTGAAAAAATTGGACACT 1379

Qy        308 Gly------SerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArg 325
Db       1380 TCTACGCTGTCCCTACAAAGGCCTGAAGACTTCCTGGACGCAGTATCTAATATATCGCGC 1439

Qy        326 ValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeu 345
Db       1440 CTACATCATCCTAACATTACAGAACTAGTGGGTTATTGCACAGAACATGAGCAATACCTT 1499

Qy        346 LeuValTyrGluPheValProAsnAsnAsnLeu------GluLeuHisLeuHisGlyGlu 363
Db       1500 CTTGTGTATGAATATTTCGACAATGGATCACTCTATGACGTATTGCACATGGCAGATGAG 1559

Qy        364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
Db       1560 ACTACTAGAAATTTGTCTTGGAACATTCGTGTAAAGATTGCGCTGGGTTCAGCTCGAGTT 1619

Qy        384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
Db       1620 TTAGAGTATTTGCATGAAGTTTGCTCTCCATCTATTGTGCATAAAAAATTCAAGTCGTCT 1679

Qy        404 AsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle 423
Db       1680 AATATTTTGCTTGATGATGATTTCAACCCTCGTCTGTCCGACTGTGGAATTGCG------ 1733

Qy        424 AlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAla 443
Db       1734 GCCCTCAATCCAAATTCTGAGCGTCAGGTTCAGGTGCTGGGTTCATTTGGGTACAGTGCT 1793
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Qy        444 ProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyVal 463
              ||||||||        ||||||      |||   ||||||||||:::|||||||||||
Db       1794 CCTGAATATGTCATGTCAGGAATCTATACAATGAAGAGCGATGTGTATAGTTTTGGAGTG 1853

Qy        464 ValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAsp 483
              |||:::|||||||||:::|||||||:::|||:::|||::::::           :::
Db       1854 GTAATGCTTGAGCTTTTGACAGGCCGGAAGCCCTTGGATAGTTCAAGAACAAGGTCAGAA 1913

Qy        484 AspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPhe 503
                |||||||||   ||||||   |||   |||:::                   |||
Db       1914 CAGTCATTAGTAAGATGGGCCACCCCTCAGCTTCAT-----------------GATATT 1955

Qy        504 GluGlyLeuAla---------AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              :::   ||||||         |||     :::         |||       :::   :::
Db       1956 GATGCATTGGCAAAGATGGTTGATCCAGCTTTGAAGGGAAGTTATCCTGCAAAATCTCTC 2015

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              :::|||               |||   |||::::::                 ||||||
Db       2016 TCGCGCTTTGCTGATATTATTGCCCTCTGCATTCAGCCTGAACCAGAATTCCGTCCTCCA 2075

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||::::::|||:::||||||         :::      :::   ||||||:::
Db       2076 ATGTCTGAAGTGGTGCAAGCATTGGTTCGTATGATGCAACGGGCTAGCCTCAATAAGAGG 2135

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              |||       :::                          :::   |||:::|||
Db       2136 ATGACAGGAGATGAA-------------------------ACTGCAGACCACGATCCT 2168

Qy        581 SerGlnTyr 583
              :::   |||
Db       2169 GCAGATTAT 2177

RESULT 6
US-09-228-986-7
; Sequence 7, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2432
;   TYPE: DNA
;   ORGANISM: Pinus radiata
US-09-228-986-7

Alignment Scores:
Pred. No.:              2.44e-20      Length:         2432
Score:                  678.00        Matches:        147
Percent Similarity:     63.05%        Conservative:   68
Best Local Similarity:  43.11%        Mismatches:     104
Query Match:            19.64%        Indels:         22
DB:                     4             Gaps:           8

US-10-086-464-2 (1-647) x US-09-228-986-7 (1-2432)

Qy        254 LeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsn 273
              :::   ||||||      |||      |||::::::::::||||||      :::||||||
Db       1046 ATTTGTCTAGGGCATTTGAAG---AGATTCTCATTCAAAGAGTTACGTGTTTCCACTAAT 1102

Qy        274 GlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyVal 293
              |||||      |||:::||||||   ||||||:::|||   |||:::||||||
Db       1103 AATTTTAGTAGCAAGAATATTTTAGGAGTAGGAGGATATGGAATTGTCTATAAAGGATTC 1162

Qy        294 LeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer---GlyGlnGly 312
              |||      |||      ||||||:::|||:::||||||   |||:::   |||   |||
Db       1163 CTACAAGATGGCACTATAGTAGCAATAAAAAGGTTGAAAGATGGTAATGTGGGAGGAGGA 1222

Qy        313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
              |||   :::||||||   |||||||||:::||||||        ||||||:::|||:::
Db       1223 GAAATTCAATTTCAAACAGAGGTGGAAATGATCAGCTTGGCTGTGCATAGGAACCTATTA 1282

Qy        333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
                 |||   |||:::|||            :::|||||||||||||||   ::::::|||
Db       1283 CGATTGTATGGATTTTGCACAACCTCCAGAGAGAGGCTTCTGGTCTATCCCTACATGCCA 1342

Qy        353 AsnAsnAsnLeuGlu------LeuHisLeuHisGlyGluGlyArgProThrMetGluTrp 370
              |||   ::::::         |||       |||       |||:::      ::::::|||
Db       1343 AATGGAAGTGTGGCCTCTTGTCTTAGAGATCATATTAATGGAAAGCTTGCCCTGGACTGG 1402

Qy        371 SerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAsp 390
                 ||||||   :::||||||||||||:::|||:::||||||   ||||||||||
Db       1403 CCTACTCGCAAGCGTATAGCCCTTGGAGCAGCTAGGGGACTGTTATATTTGCATGAGCAA 1462

Qy        391 CysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLys 410
              |||:::|||||||||||||||||||:::|||||:::||||||||:::|||
Db       1463 TGTGATCCCAAGATTATTCACCGGGATGTGAAAGCAGCAAATATATTACTGGATGAATAT 1522

Qy        411 PheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHis 430
              |||||||||   |||   |||||||||||||||||:::             ::::::|||
Db       1523 TTTGAAGCTGTTGTTGGAGATTTTGGGTTAGCAAAGCTCTTGGATCACAGGGATTCTCAT 1582

Qy        431 ValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGly 450
              |||:::|||   |||   ||||||   |||:::::|||||||||||   ::::::|||
Db       1583 GTGACTACTGCTGTTCGAGGGACGGTAGGTCACATTGCCCCAGAATACCTTTCAACGGGA 1642

Qy        451 LysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThr 470
              :::   :::||||||:::||||||||   ||||||:::::|||||||||||||||||||
Db       1643 CAATCTTCAGAGAAAACTGATGTATTTGGCTTTGGGATATTACTGTTGGAACTCATTACA 1702

Qy        471 GlyArgArgProValAsp-----------AlaAsnAsnValTyrValAspAspSerLeu 486
              |||:::|||   :::|||           |||           |||         :::
Db       1703 GGACAAAGGGCTTTAGATTTTGGCCAGGCTGCAAAGCAAAAAGTTGTA---------ATG 1753

Qy        487 ValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeu 506
              :::||||||   :::   |||             ::::::             |||
Db       1754 CTGGATTGGGTAAAGAAGCTT-----------CATCAAGAGAAGAAGTTGCACCTCCTT 1801

Qy        507 AlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCys 526
              ||||||      :::         :::||||||   |||:::      ||||||
Db       1802 GCTGATAAAGATCTTAAGGGCAATTTTGATAGAGTTGAGCTAGAAGAGATGGTTCAGGTT 1861

Qy        527 AlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArg 546
              :::       |||   :::                 |||||:::|||      ::::::|||
Db       1862 TCTTTGCTATGCACCCAATTTCAGCCTGGACATCGTCCAAAAATGTGTGATGTTTTGAGA 1921

Qy        547 AlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSer 566
                 |||||||:::      |||::::::      |||   ::::::      ::::::
Db       1922 ATGTTGGAAGGTGAT---GGATTGACAGAACGGTGGGAAACATTGCAAAAAATTGAAACC 1978

Qy        567 AsnValTyrSer-----------------SerTyrGlyGlySerThrAspTyrAspSer 580
                  |||                     :::|||           :::   ||||||
Db       1979 CCCCGATACAGAGTAACTGAGATACCCATAACATATTCCGAGTTGGTTGAAGAAGATTCT 2038

Qy        581 Ser 581
              |||
Db       2039 TCT 2041

RESULT 7
US-09-602-472A-3
; Sequence 3, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
;  APPLICANT: Bidney, Dennis L.
;  APPLICANT:  Hu, Xu
;  APPLICANT:  Li, Guihua
;  TITLE OF INVENTION: Sunflower Disease Resistance Genes
;  FILE REFERENCE: 35718/200630
;  CURRENT APPLICATION NUMBER: US/09/602,472A
;  CURRENT FILING DATE:  2000-06-23
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;  PRIOR APPLICATION NUMBER: 60/140,876
;  PRIOR FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1559
;   TYPE: DNA
;   ORGANISM: Helianthus annuus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (81)...(1319)
US-09-602-472A-3

Alignment Scores:
Pred. No.:              4.39e-20      Length:         1559
Score:                  667.50        Matches:        165
Percent Similarity:     57.50%        Conservative:   65
Best Local Similarity:  41.25%        Mismatches:     117
Query Match:            19.33%        Indels:         57
DB:                     4             Gaps:           9

US-10-086-464-2 (1-647) x US-09-602-472A-3 (1-1559)

Qy        219 SerProProArgGlnProProProProProProProProPheMetSerSerSerGlyGly 238
              ||||||     :::|||      ||||||  ||||||
Db        131 TCACCAAAAAGTCGGCCATGAAGTCCACCCAT-CCGCCCCTT----------------- 171

Qy        239 SerAspTyrSerAspArgProValLeuProProProSerProGlyLeuVal--------- 255
                              |||:::   |||         |||||||||:::
Db        172 ------------------CCAATATTTCCAGATTATCTTCCGGGGTTGATAGGATGAAAA 213

Qy        255 ------------------------------------------------------------ 255

Db        214 CGAGAAACAATGTTAATAATGCTGCTAGCCTAAGGAGGGAGTCATCAGGGCCGCCGGATG 273

Qy        256 LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPhe 275
              |||      :::      |||||||||:::   |||||||||   |||||||||   |||
Db        274 CTCAA-ATCGCCGCACAAACCTTCACATTCCGCGAGCTTGCAGCCGCCACCAATAATTTT 332

Qy        276 SerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu--- 294
                          |||   :::|||||||||||||   |||:::::|||   |||
Db        333 CAGCCTGATTGCTTCTTAAGGGAGGGTGGTTTTGGTTGTGTATATAGAGGACGTCTTCAG 392

Qy        295 ProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArg 314
              ||||||:::   |||||||||||||||||||                 ||||||   |||
Db        393 AGTAGTGGTCAAGTTGTAGCTGTTAAACAGCTGGATAGAAATGGACTCCAAGGTAACCGT 452

Qy        315 GluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeu 334
              ||||||     ||||||   :::::::|||   :::||||||   :::||||||:::|||
Db        453 GAGTTTCTTGTTGAAGTTCTTATGCTCAGCCTTTTACATCATCCAAACTTGGTCAATTTG 512

Qy        335 ValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsn 354
              :::||||||||||      |||   :::|||||||||||||||||||||:::
Db        513 ATTGGCTACTGCGCTGACGGTGACCAACGACTTCTTGTCTATGAGTTTATGGCCTTGGGT 572

Qy        355 AsnLeuGluLeuHisLeuHisGly------GluGlyArgProThrMetGluTrpSerThr 372
              :::||||||   |||||||||                  |||      ::::::|||   |||
Db        573 TCCTTGGAAGATCACCTTCATGATGTTCCGCCTGACAGAGAACCATTAGATTGG---ACA 629

Qy        373 -ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAs 392
               |||:::|||||||||      :::||||||||||||   :::||||||:::      ||
Db        630 CAGGATGAAGATAGCGGCTGT-GCAGCCAAGGGGTTGGAGTTTCTTCATGATAAAGCTAA 688

Qy        392 nProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGl 412
              ||||   :::|||:::||||||   |||:::||||||||||||:::|||      |||::
Db        689 CCCACCAGTTATTTATCGGGACTTCAAATCATCAAACATTTTGCTGGATGAGGGATTTCA 748

Qy        412 uAlaLysValAlaAspPheGlyLeuAlaLysIleAla---SerAspThrAsnThrHisVa 431
              :   |||::::::|||||||||||||||||||:::      :::          :::|||||
Db        749 ACCAAAGCTGTCCGACTTCGGGCTCGCGAAACTGGGCCCCACTGGAGACAAGTCTCATGT 808

Qy        431 lSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLy 451
              |||||||||||||||||||||:::||||||   ||||||||||||||   :::|||::
Db        809 TTCCACACGGGTGATGGGTACATACGGTTACTGTGCTCCTGAGTATGCCATGACTGGTCA 868

Qy        451 sLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGl 471
              :||||||   ||||||||||||:::||||||||||||||||   ||||||||||||||||
Db        869 GTTAACGGTCAAATCCGATGTGTACAGCTTTGGTGTCGTCTTTTTAGAGCTTATTACCGG 928

Qy        471 yArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaAr 491
              ||||:::   :::|||:::          :::          :::|||||||   ||||||||
Db        929 TAGAAAAGCCATAGATAGCACTCAACCACATGGACAGCAGAACCTGGTGACATGGGCACG 988

Qy        491 gProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMe 511
              |||||||   |||         ::::::      |||      |||   |||   :::::
Db        989 ACCTTTGTTCAAC---------GACAGAAGGAAATTCACATCGTTGGTGGACCCACGGTT 1039

Qy        511 tAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVa 531
              :          |||         :::   :::   :::|||   |||:::   |||::
Db       1040 AGAAGGTCGGTACCCAATGCGGGGGCTGTACCAGGCGCTAGCGGTGGCATCCATGTGTAT 1099

Qy        531 lArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAs 551
              ::::                |||||||   ::::::   :::|||   ||||||
Db       1100 TCAAGAACAGGTTGCAGCCCGGCCTTTGATTGCTGACGTGGTAACTGCGCTATCTTATCT 1159

Qy        551 nValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSer------------As 567
                                  |||:::|||      |||      |||            ||
Db       1160 TGCA--------------AACCAGGGGTACGATCCGAC-CACAGCTCCCAGCTTCATAA 1203

Qy        567 nValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAsp 586
              |:::   ||||||   ||||||                  ::::::::::::::::::::
Db       1204 CATCATCAGCAGCGCCGGCGGCAAGGAGAGACTTAAAACCGCAAGGTTTTCGAAAAAC 1261

RESULT 8
US-08-881-706-1
; Sequence 1, Application US/08881706
; Patent No. 6245969
; GENERAL INFORMATION:
;  APPLICANT: Chong, Joane
;  APPLICANT: Li, Jianming
;  TITLE OF INVENTION: Receptor Kinase BIN1
;  FILE REFERENCE: 07251/022001
;  CURRENT APPLICATION NUMBER: US/08/881,706
;  CURRENT FILING DATE: 1997-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4104
;   TYPE: DNA
;   ORGANISM: Arabidopsis sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(3687)
US-08-881-706-1

Alignment Scores:
Pred. No.:              4.4e-17       Length:         4104
Score:                  604.50        Matches:        161
Percent Similarity:     47.21%        Conservative:   84
Best Local Similarity:  31.02%        Mismatches:     148
Query Match:            17.51%        Indels:         127
DB:                     3             Gaps:           14

US-10-086-464-2 (1-647) x US-08-881-706-1 (1-4104)

Qy        107 ProPro------------SerAsnProSerArgGluGlyGlySerProArgProProSer 122
              ||||||               :::||||||      |||   |||   |||
Db       2350 CCACCGGCTAAGTTCTTGAACAATCCTGGTCTC---TGTGGTTATCCTCTTCCGCGGTGT 2406

Qy        123 SerProSerProProSerProSerSerAspGlyLeu--------------SerThrGly 137
                  ||||||             ::::::||||||               |||   |||
Db       2407 GATCCTTCA------------AATGCAGACGGTTATGCTCATCATCAGAGATCTCATGGA 2454

Qy        138 ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCys 157
                                  |||   ||||||:::   ::::::   :::   :::|||
Db       2455 AGGAGACCAGCGTCCCTTGCTGGTAGTGTGGCGATGGGATTGTTGTTCTCTTTTGTGTGT 2514
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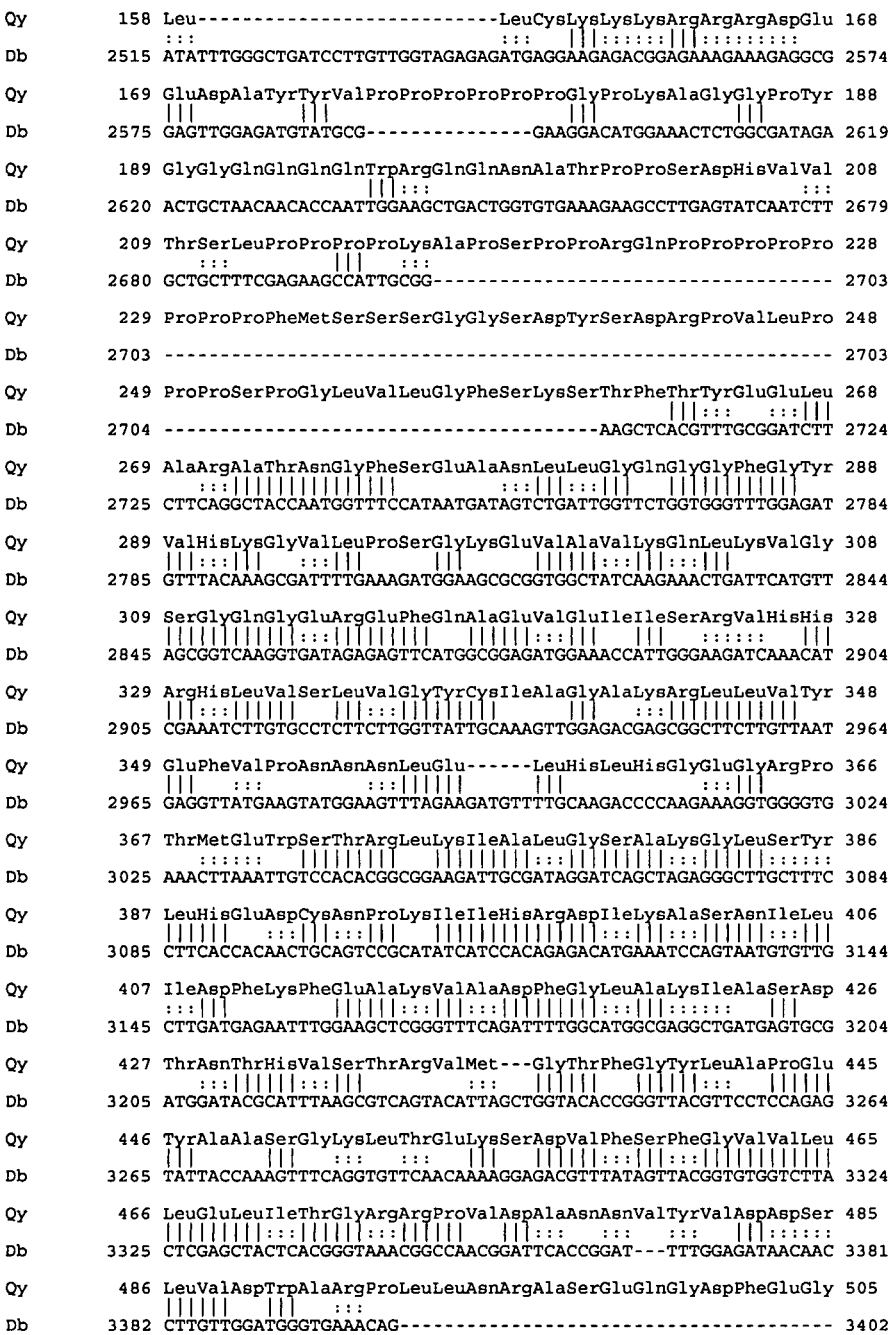

RESULT 9
US-09-579-182-3
; Sequence 3, Application US/09579182
; Patent No. 6500628
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-161
; CURRENT APPLICATION NUMBER: US/09/579,182
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-579-182-3

Alignment Scores:

Pred. No.:	1.81e-17	Length:	1224
Score:	602.00	Matches:	153
Percent Similarity:	48.41%	Conservative:	60
Best Local Similarity:	34.77%	Mismatches:	157
Query Match:	17.43%	Indels:	70
DB:	4	Gaps:	9

US-10-086-464-2 (1-647) x US-09-579-182-3 (1-1224)

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Qy        236 SerGlySerAspTyrSerAspArgProValLeuProProProSerPro------Gly 253
Db        364 AAAGACGGATCGAGCGTATCTTCTGCTAATCCTTTGACAGCTCCATCTCCTTTGTCTGGT 423

Qy        254 LeuVal-----------LeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAla 269
Db        424 CTTCCTGAGTTTTCTCACCTTGGATGGGGA---CATTGGTTCACTCTTAGAGATCTTCAG 480

Qy        270 ArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrVal 289
Db        481 ATGGCTACTAATCAGTTTTCAAGGGATAATATCATCGGTGATGGTGGATATGGAGTTGTT 540

Qy        290 HisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySer 309
Db        541 TACCGCGGTAACCTTGTTAATGGTACTCCTGTTGCTGTTAAAAAGTTGCTCAACAATTTA 600

Qy        310 GlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArg 329
Db        601 GGACAAGCTGATAAAGACTTCAGAGTTGAAGTTGAAGCTATAGGTCACGTTCGACATAAA 660

Qy        330 HisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGlu 349
Db        661 AACTTGGTCCGCCTTCTCGGATATTGTATGGAAGGAACGCAGAGG--------------- 705

Qy        350 PheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGlu 369
Db        705 ------------------------------------------------------------ 705

Qy        370 TrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGlu 389
Db        706 ----------------------------------------CTCGCGTACCTTCACGAG 723

Qy        390 AspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPhe 409
Db        724 GCGATTGAGCCAAAAGTGGTGCACAGAGACATTAAGTCTAGTAACATTCTGATTGATGAC 783

Qy        410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThr 429
Db        784 AAATTCAATTCTAAAATTTCTGACTTTGGACTTGCTAAACTACTTGGTGCTGATAAGAGT 843

Qy        430 HisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSer 449
Db        844 TTTATAACTACTAGAGTTATGGGTACCTTCGGTTACGTAGCTCCAGAGTATGCGAATTCC 903

Qy        450 GlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIle 469
Db        904 GGTCTTCTGAATGAGAAAAGCGATGTCTACAGCTTCGGGGTTGTACTCTTGGAAGCTATA 963

Qy        470 ThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrp 489
Db        964 ACTGGTAGATATCCGGTAGACTATGCTCGTCCACCACCCGAGGTACATTTGGTGGAGTGG 1023

Qy        490 AlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAla 509
Db       1024 CTGAAGATGATGGTC-----------CAACAAAGACGATCAGAAGAAGTGGTTGATCCA 1071

Qy        510 LysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAla 529
Db       1072 AACCTTGAAACAAAACCATCTACAAGTGCTTTGAAAAGAACACTATTGACTGCTTTGAGA 1131

Qy        530 CysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGlu 549
Db       1132 TGTGTTGATCCAATGTCTGAGAAAAGACCGAGGATGAGCCAAGTTGCACGTATGCTTGAA 1191

RESULT 10
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-09-228-986-11

Alignment Scores:
Pred. No.:                4.95e-17      Length:          3097
Score:                    600.50        Matches:         173
Percent Similarity:       46.08%        Conservative:    80
Best Local Similarity:    31.51%        Mismatches:      172
Query Match:              17.39%        Indels:          126
DB:                       4             Gaps:            13

US-10-086-464-2 (1-647) x US-09-228-986-11 (1-3097)

Qy         66 ProSerThrProGlySerProProPro--------------------------LeuPro 76
Db       1523 CCTGCAAGTTCTGGACGTCCAAAACAACAGCTTAGACGGAGTTGTTCCCGACGGCTTGGG 1582

Qy         77 GlnProSerProProAlaProThrThrProGlySerProProAlaProValThrPro--- 95
Db       1583 AGAGCTGAAAGACCTTCACCTACTGGACTTGGAGAATAACCTGCTACAAG-GTACCTTAC 1641

Qy         96 --------------------ProThrArgAsnProProProSerValProGlyProPro 108
Db       1642 CAGATTCCTTGAACAGACAGAGCTTGGAGGTCAGAACCTCAGGAAACTTGTGTCTTTCCT 1701

Qy        109 SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerPro------ 126
Db       1702 TCTCCACAACCGCGTGC-GGTGATGCATCATCTAGTCCTTCAATTGAGGCACCGCAAGTT 1760

Qy        127 ---------ProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAla 143
Db       1761 ACAATAGTTCCCGAGAGAAACAAAGGGGGACATAATCGTTTAGCCATTATACTCGGAGCA 1820

Qy        144 IleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLys 163
Db       1821 GTCGGAGGAGTATCACTAGCTATTTTACTCATCCCGCTCTTCGTATTCATGTACAGAAGG 1880

Qy        164 ArgArgArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLys 183
Db       1881 AGAGGAAGAACTGAA---------------------------------------------- 1895

Qy        184 AlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProPro 203
Db       1895 ------------------------------------------------------------ 1895

Qy        204 SerAspHisValValThrSerLeuProProProProLysAlaProSerProProArgGln 223
Db       1895 ------------------------------------------------------------ 1895

Qy        224 ProProProProProProProProPheMetSerSerSerGlyGlySerAspTyrSerAsp 243
Db       1896 ----------------------------------------ATGTCATATACGGAA 1910

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
Db       1911 AGGGCAGTCGCAGACGTGAGAAACTGGAAT--------------GCAGCTAAGATTTTT 1955

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
Db       1956 TCCTACAAAGAGATCAAAACAGCTACAAACAACTTTAAAGAA------GTCATTGGTCAT 2009

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
Db       2010 GGAAGTTTTGGATCCGTGTACCTGGGAAACCTTCCAGTTGGAAAACTAGTTGCTGTGAAA 2069
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```
Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
                          :::      |||        |||      ||||||   ::::::
Db       2070 GTGCGGTTTGATAAAACCCAACTTGGTGCAGATTCTTTCATAAATGAGGTTCGTCTCTTA 2129

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
              |||:::|||   |||::::::||||||||||||   |||:::|||             :::
Db       2130 TCACAAGTCCGCCATCAGAACCTTGTCAGTCTGGAAGGATTTTGTTATGAGTCGCAGCGT 2189

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGlu 363
              ::::::||||||||||||::::::|||      :::|||          |||:::|||
Db       2190 CAGATTTTAGTCTATGAATATCTACCGGGTGGATCACTGGCTGATCAACTGTATGGTCCA 2249

Qy        364 Gly------ArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
                  :::   ::::::   |||      ||||||||||||||:::   :::|||
Db       2250 AACAGTAGGAAATTCTCACTAAGCTGGGTTCGTAGACTCAAGATTGCTGTTGATGCTGCA 2309

Qy        382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
              |||||||||   |||||||||         ||||||:::||||||||||||||||||||
Db       2310 AAAGGACTGGACTATCTACATAATGGAAGCAATCCTCGAATCATACACCGAGACATCAAG 2369

Qy        402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
                |||||||||||:::|||   :::      |||::::::   |||||||||||:::
Db       2370 TGCAGTAATATACTATTGGACAAGGAGATGAATGCAAGACTTTGCGACTTTGGGCTCTCT 2429

Qy        422 Lys------IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPhe 439
              |||      |||     |||     |||||||||:::|||   |||   ||||||
Db       2430 AAGCAAATGATCCAGCCAGACGCA---ACTCACGTGACCACTGTCGTCAAGGGCACAGCT 2486

Qy        440 GlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPhe 459
              |||||||||   |||||||||   ::::::   :::||||||||||||||||||:::
Db       2487 GGTTACCTCGACCCTGAATATTACTCCACCCAACAACTTACAGAGAAAAGCGACGTCTAT 2546

Qy        460 SerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsn 479
              ||||||||||||||||||||||||||||   ||||||   |||::::::   :::
Db       2547 AGCTTTGGAGTTGTGCTTTTGGAGCTCATCTGTGGACGAGAGCCGTTAAATCATTCAGGA 2606

Qy        480 ValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGlu 499
                      :::|||||||   ||||||:::|||   |||             :::
Db       2607 ACTCCAGATTCCTTCAATTTGGTTTTATGGGCAAAGCCCTACTTG-----------CAG 2654

Qy        500 GlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGlu 519
              |||   ||||||   :::   |||      :::         :::|||   |||
Db       2655 GCAGGTGCATTTGAG---ATAGTGGATGAGAGTTTAGGGGGAAGTTTCGATGTGGAAAGC 2711

Qy        520 MetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgPro 539
              |||   ::::::          |||          |||          |||      ||||||
Db       2712 ATGAGGAAAGTGGCAAAAATCGCTGTGAGGTCTGTAGAGAGGGATGCATCACTAAGGCCA 2771

Qy        540 ArgMetSerGlnIleValArgAlaLeuGluGly------AsnValSerLeuSerAspLeu 557
                ::::::||||||:::      |||:::        ::::::   ||||||
Db       2772 ACCATTGCACAGATACTGTCTGTGCTCAAAGAGGCTTACAGCATTCAGCTCTCT------ 2825

Qy        558 AsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAsp 577
                                                |||   :::      |||      :::
Db       2826 --------------------------------TATCTTGCAGCCTCTGGACATGTGAAC 2852

Qy        578 TyrAspSerSerGlnTyrAsnGluAsp 586
                    |||   ||||||:::|||
Db       2853 TGAATCTACTCGTATTACAACCAAGAC 2879
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RESULT 11
US-08-587-889-1
; Sequence 1, Application US/08587889
; Patent No. 5654397
; GENERAL INFORMATION:
; APPLICANT: CAO, Zhaodan
; APPLICANT: CROSTON, Glenn E.
; APPLICANT: GOEDDEL, David V.
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR-ASSOCIATED
; TITLE OF INVENTION: PROTEIN KINASE AND BINDING ASSAY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,889
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-60916
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3590 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-587-889-1

Alignment Scores:

Pred. No.:	3.48e-16	Length:	3590
Score:	581.50	Matches:	208
Percent Similarity:	38.68%	Conservative:	86
Best Local Similarity:	27.37%	Mismatches:	239
Query Match:	16.84%	Indels:	229
DB:	1	Gaps:	28

US-10-086-464-2 (1-647) x US-08-587-889-1 (1-3590)

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Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
              |||:::      |||   ||| |||:::      ||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla------------------------ProProPr 32
              |          |||         :::|||                              |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro------------------------------------ 39
              ||||       ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                  |||   |||      |||   |||      |||   |||   :::||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro------------------------------ThrProSerTh 68
              |||                                                |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
              ||||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
              |||   |||   :::   ||||||          |||   |||       ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519
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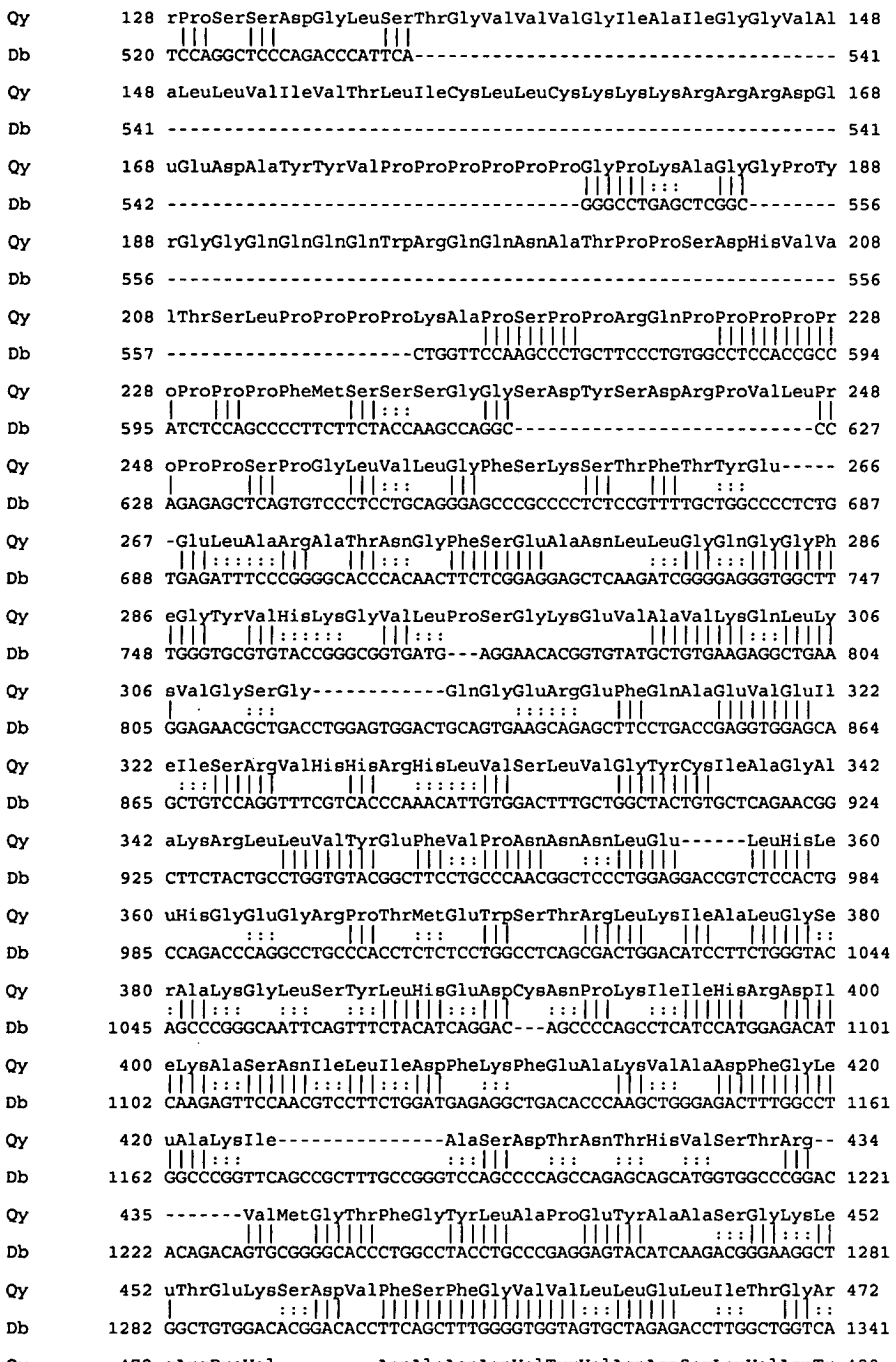

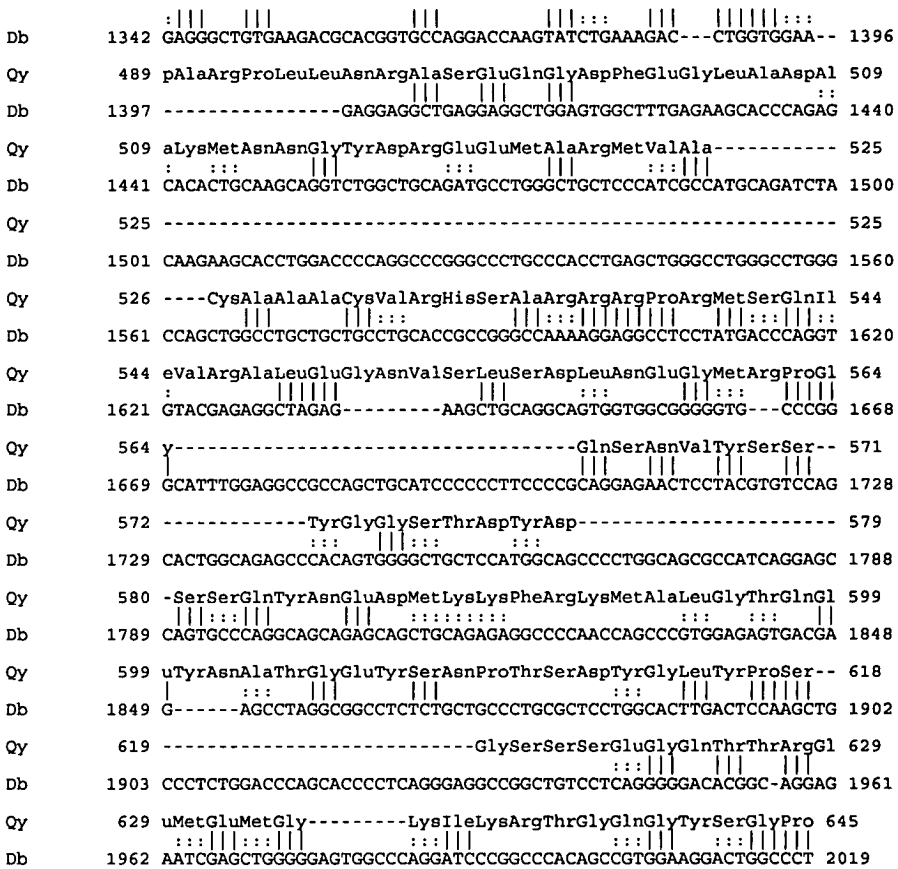

RESULT 12
US-09-016-434-1093
; Sequence 1093, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:

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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1093:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3590 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1220312
US-09-016-434-1093

Alignment Scores:
Pred. No.:              3.48e-16      Length:         3590
Score:                  581.50        Matches:        208
Percent Similarity:     38.68%        Conservative:   86
Best Local Similarity:  27.37%        Mismatches:     239
Query Match:            16.84%        Indels:         229
DB:                     4             Gaps:           28

US-10-086-464-2 (1-647) x US-09-016-434-1093 (1-3590)

Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
              |||:::      |||   ||| |||:::      ||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla------------------------ProProPr 32
              |      |||         :::|||                             |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro----------------------------------- 39
              ||||     ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                  |||   |||       |||   |||       |||   |||   :::||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro------------------------------ThrProSerTh 68
              |||                                               |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
              ||||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
              |||   |||   :::   ||||||          |||   |||       ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148
              |||   |||         |||
Db        520 TCCAGGCTCCCAGACCCATTCA---------------------------------- 541

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db        541 ------------------------------------------------------------ 541

Qy        168 uGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTy 188
                                                      ||||||:::   |||
Db        542 ----------------------------------GGGCCTGAGCTCGGC-------- 556

Qy        188 rGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValVa 208

Db        556 ------------------------------------------------------------ 556

Qy        208 lThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPr 228
                                       |||||||||           ||||||||||
Db        557 ---------------------CTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCC 594

Qy        228 oProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuPr 248
              |   |||         |||:::      |||                            ||
Db        595 ATCTCCAGCCCCTTCTTCTACCAAGCCAGGC-------------------------CC 627

Qy        248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu----- 266
              |   |||      |||:::  |||        |||  |||  :::
Db        628 AGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTCTCCGTTTTGCTGGCCCCTCTG 687

Qy        267 -GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPh 286
               |||::::::|||   |||:::  |||||||||         :::|||:::||||||||
Db        688 TGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAGGGTGGCTT 747

Qy        286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306
              ||||   |||:::::  |||:::                    |||||||||:::|||||
Db        748 TGGGTGCGTGTACCGGGCGGTGATG---AGGAACACGGTGTATGCTGTGAAGAGGCTGAA 804

Qy        306 sValGlySerGly------------GlnGlyGluArgGluPheGlnAlaGluValGluIl 322
              |     :::                  ::::::   |||      |||||||||
Db        805 GGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTGGAGCA 864

Qy        322 eIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342
              :::||||||      |||   ::::::|||      ||||||||
Db        865 GCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAGAACGG 924

Qy        342 aLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLe 360
                  |||||||||   |||:::||||||   :::||||||      ||||||
Db        925 CTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTCCACTG 984

Qy        360 uHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380
                    :::      |||   :::   |||      ||||||   |||   ||||||::
Db        985 CCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTGGGTAC 1044

Qy        380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIl 400
              :|||:::   :::   :::||||||:::|||   :::|||   :::||||||   |||||
Db       1045 AGCCCGGGCAATTCAGTTTCTACATCAGGAC---AGCCCCAGCCTCATCCATGGAGACAT 1101

Qy        400 eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420
              ||||:::||||||:::|||:::|||   :::          |||:::   ||||||||||
Db       1102 CAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGCCT 1161

Qy        420 uAlaLysIle---------------AlaSerAspThrAsnThrHisValSerThrArg-- 434
              ||||:::                 :::|||   :::   :::   :::      |||
Db       1162 GGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGGAC 1221

Qy        435 -------ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452
                    |||   ||||||      ||||||      ||||||      :::|||:::||
Db       1222 ACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGGCT 1281

Qy        452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472
              |         :::|||   ||||||||||||||||||:::||||||   :::   |||::
Db       1282 GGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGTCA 1341

Qy        472 gArgProVal---------AspAlaAsnAsnValTyrValAspAspSerLeuValAspTr 489
              :|||   |||           |||      |||:::   |||   ||||||:::
Db       1342 GAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGAC---CTGGTGGAA-- 1396

Qy        489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509
                                      |||   |||   |||                ::
Db       1397 ---------------GAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAG 1440

Qy        509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAla----------- 525
              :   :::      |||         :::      |||      :::|||
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Db       1441 CACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTA 1500

Qy        525 ------------------------------------------------------------ 525

Db       1501 CAAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGG 1560

Qy        526 ----CysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544
                   |||      |||:::         |||:::|||||||||   |||:::|||::
Db       1561 CCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGT 1620

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564
                :      ||||||           |||      :::      |||:::   |||||
Db       1621 GTACGAGAGGCTAGAG---------AAGCTGCAGGCAGTGGTGGCGGGGGTG---CCCGG 1668

Qy        564 y-----------------------------------GlnSerAsnValTyrSerSer-- 571
                                                  |||   |||   |||   |||
Db       1669 GCATTTGGAGGCCGCCAGCTGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAG 1728

Qy        572 ------------TyrGlyGlySerThrAspTyrAsp---------------------- 579
                         :::   |||:::      :::
Db       1729 CACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGC 1788

Qy        580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGl 599
                |||:::|||      |||   :::::::::               :::   :::   ||
Db       1789 CAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGA 1848

Qy        599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618
                |      :::   |||      |||              :::   |||   ||||||
Db       1849 G------AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG 1902

Qy        619 ---------------------------GlySerSerSerGluGlyGlnThrThrArgGl 629
                                          :::|||   |||   |||
Db       1903 CCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGC-AGGAG 1961

Qy        629 uMetGluMetGly---------LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645
                :::|||:::|||         :::|||          :::|||   :::||||||
Db       1962 AATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCT 2019

RESULT 13
PCT-US96-09193-1
; Sequence 1, Application PC/TUS9609193
;  GENERAL INFORMATION:
;    APPLICANT:  Tularik, Inc.
;    TITLE OF INVENTION:  INTERLEUKIN-1 RECEPTOR-ASSOCIATED
;    TITLE OF INVENTION:  PROTEIN KINASE AND BINDING ASSAY
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
;      STREET:  4 Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09193
;      FILING DATE:  JUNE 5 1996
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. Serial No. 08/587,889
;      FILING DATE:  JAN 16 1996
;      CLASSIFICATION:
;      APPLICATION NUMBER:  U.S. Serial No. 08/494,006
;      FILING DATE:  JUNE 23 1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David J. Brezner
;      REGISTRATION NUMBER:  24,774
;      REFERENCE/DOCKET NUMBER:  FP-62191-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 494-8700
;      TELEFAX:  (415) 494-8771
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3590 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US96-09193-1

Alignment Scores:
Pred. No.:              3.48e-16        Length:         3590
Score:                  581.50          Matches:        208
Percent Similarity:     38.68%          Conservative:   86
Best Local Similarity:  27.37%          Mismatches:     239
Query Match:            16.84%          Indels:         229
DB:                     5               Gaps:           28

US-10-086-464-2 (1-647) x PCT-US96-09193-1 (1-3590)

Qy          1 MetSerSerAlaProSerPro-GlyThrGlySerProProSerProProSerAsnSerTh 20
                |||:::      |||   ||| |||:::      ||||||:::|||   ::::::   ||
Db         80 ATGGCCGGGGGGCCGGGCCCGGGGGAGCCCGCAGCCCCCGGCGCCCAGCACTTCTTGTAC 139

Qy         20 rThrThrThrProProProAlaSerAla-----------------------ProProPr 32
                |          |||          :::|||                           |||||
Db        140 GAGGTGCCGCCCTGGGTCATGTGCCGCTTCTACAAAGTGATGGACGCCCTGGAGCCCGCC 199

Qy         32 oThrThrProSerSerProPro---------------------------------------- 39
                ||||      ||||||||||||
Db        200 GACTGGTGCCAGTTCGCCGCCCTGATCGTGCGCGACCAGACCGAGCTGCGGCTGTGCGAG 259

Qy         40 ----ProProSerThrIleProThrSerProProProSerSerArgSerThrProSerAl 58
                   |||   |||      |||   |||      |||   |||   :::|||||||
Db        260 CGCTCCGGGCAGCGCACGGCCAGCGTCCTGTGGCCCTGGATCAACCGCAACGCCCGTGTG 319

Qy         58 aProProProSerProPro-------------------------------ThrProSerTh 68
                |||                                             |||   |||
Db        320 GCCGACCTCGTGCACATCCTCACGCACCTGCAGCTGCTCCGTGCGCGGGACATCATCACA 379

Qy         68 rProGlySerProProProLeuProGlnProSerProProAlaProThrThrProGlySe 88
                ||||||:::   ||||||      :::|||      |||   |||
Db        380 GCCTGGCACCCTCCCGCCCCGCTTCCGTCCCCAGGCACCACTGCCCCGA---------GG 430

Qy         88 rProProAlaProValThrProProThrArgAsnProProProSerValProGlyProPr 108
                |||   |||   :::   ||||||          |||   |||      ||||||
Db        431 CCCAGCAGCATCCCTGCACCCGCCG------AGGCCGAGGCCTGGAGCCCCCGGA----- 479

Qy        108 oSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSe 128
                                          |||:::||||||   |||   ||||||
Db        480 ------------------AGTTGCCATCCTCAGCCTCCACCTTCCTC-TCCCCAGCTTT 519

Qy        128 rProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAl 148
                |||   |||         |||
Db        520 TCCAGGCTCCCAGACCCATTCA---------------------------------------- 541

Qy        148 aLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGl 168

Db        541 ------------------------------------------------------------ 541

Qy        168 uGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyProTy 188
                                                  ||||||:::   |||
Db        542 ----------------------------------GGGCCTGAGCTCGGC-------- 556

Qy        188 rGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValVa 208

Db        556 ------------------------------------------------------------ 556

Qy        208 lThrSerLeuProProProProLysAlaProSerProProArgGlnProProProProPr 228
                                         |||||||||          ||||||||||
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Db        557 ----------------------CTGGTTCCAAGCCCTGCTTCCCTGTGGCCTCCACCGCC 594

Qy        228 oProProProPheMetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuPr 248

Db        595 ATCTCCAGCCCCTTCTTCTACCAAGCCAGGC--------------------------CC 627

Qy        248 oProProSerProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGlu----- 266

Db        628 AGAGAGCTCAGTGTCCCTCCTGCAGGGAGCCCGCCCCTCTCCGTTTTGCTGGCCCCTCTG 687

Qy        267 -GluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPh 286

Db        688 TGAGATTTCCCGGGGCACCCACAACTTCTCGGAGGAGCTCAAGATCGGGGAGGGTGGCTT 747

Qy        286 eGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLy 306

Db        748 TGGGTGCGTGTACCGGGCGGTGATG---AGGAACACGGTGTATGCTGTGAAGAGGCTGAA 804

Qy        306 sValGlySerGly------------GlnGlyGluArgGluPheGlnAlaGluValGluIl 322

Db        805 GGAGAACGCTGACCTGGAGTGGACTGCAGTGAAGCAGAGCTTCCTGACCGAGGTGGAGCA 864

Qy        322 eIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAl 342

Db        865 GCTGTCCAGGTTTCGTCACCCAAACATTGTGGACTTTGCTGGCTACTGTGCTCAGAACGG 924

Qy        342 aLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGlu------LeuHisLe 360

Db        925 CTTCTACTGCCTGGTGTACGGCTTCCTGCCCAACGGCTCCCTGGAGGACCGTCTCCACTG 984

Qy        360 uHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySe 380

Db        985 CCAGACCCAGGCCTGCCCACCTCTCTCCTGGCCTCAGCGACTGGACATCCTTCTGGGTAC 1044

Qy        380 rAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIl 400

Db       1045 AGCCCGGGCAATTCAGTTTCTACATCAGGAC---AGCCCCAGCCTCATCCATGGAGACAT 1101

Qy        400 eLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLe 420

Db       1102 CAAGAGTTCCAACGTCCTTCTGGATGAGAGGCTGACACCCAAGCTGGGAGACTTTGGCCT 1161

Qy        420 uAlaLysIle--------------AlaSerAspThrAsnThrHisValSerThrArg-- 434

Db       1162 GGCCCGGTTCAGCCGCTTTGCCGGGTCCAGCCCCAGCCAGAGCAGCATGGTGGCCCGGAC 1221

Qy        435 -------ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLe 452

Db       1222 ACAGACAGTGCGGGGCACCCTGGCCTACCTGCCCGAGGAGTACATCAAGACGGGAAGGCT 1281

Qy        452 uThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyAr 472

Db       1282 GGCTGTGGACACGGACACCTTCAGCTTTGGGGTGGTAGTGCTAGAGACCTTGGCTGGTCA 1341

Qy        472 gArgProVal---------AspAlaAsnAsnValTyrValAspAspSerLeuValAspTr 489

Db       1342 GAGGGCTGTGAAGACGCACGGTGCCAGGACCAAGTATCTGAAAGAC---CTGGTGGAA-- 1396

Qy        489 pAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAl 509

Db       1397 ---------------GAGGAGGCTGAGGAGGCTGGAGTGGCTTTGAGAAGCACCCAGAG 1440

Qy        509 aLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAla----------- 525

Db       1441 CACACTGCAAGCAGGTCTGGCTGCAGATGCCTGGGCTGCTCCCATCGCCATGCAGATCTA 1500

Qy        525 ------------------------------------------------------------ 525

Db       1501 CAAGAAGCACCTGGACCCCAGGCCCGGGCCCTGCCCACCTGAGCTGGGCCTGGGCCTGGG 1560

Qy        526 ----CysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIl 544

Db       1561 CCAGCTGGCCTGCTGCTGCCTGCACCGCCGGGCCAAAAGGAGGCCTCCTATGACCCAGGT 1620

Qy        544 eValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArgProGl 564

Db       1621 GTACGAGAGGCTAGAG---------AAGCTGCAGGCAGTGGTGGCGGGGGTG---CCCGG 1668

Qy        564 y-----------------------------------GlnSerAsnValTyrSerSer-- 571

Db       1669 GCATTTGGAGGCCGCCAGCTGCATCCCCCCTTCCCCGCAGGAGAACTCCTACGTGTCCAG 1728

Qy        572 ------------TyrGlyGlySerThrAspTyrAsp---------------------- 579

Db       1729 CACTGGCAGAGCCCACAGTGGGGCTGCTCCATGGCAGCCCCTGGCAGCGCCATCAGGAGC 1788

Qy        580 -SerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGl 599

Db       1789 CAGTGCCCAGGCAGCAGAGCAGCTGCAGAGAGGCCCCAACCAGCCCGTGGAGAGTGACGA 1848

Qy        599 uTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSer-- 618

Db       1849 G------AGCCTAGGCGGCCTCTCTGCTGCCCTGCGCTCCTGGCACTTGACTCCAAGCTG 1902

Qy        619 ----------------------------GlySerSerSerGluGlyGlnThrThrArgGl 629

Db       1903 CCCTCTGGACCCAGCACCCCTCAGGGAGGCCGGCTGTCCTCAGGGGGACACGGC-AGGAG 1961

Qy        629 uMetGluMetGly---------LysIleLysArgThrGlyGlnGlyTyrSerGlyPro 645

Db       1962 AATCGAGCTGGGGGAGTGGCCCAGGATCCCGGCCCACAGCCGTGGAAGGACTGGCCCT 2019
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RESULT 14
US-09-602-472A-5
; Sequence 5, Application US/09602472A
; Patent No. 6608240
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Hu, Xu
; APPLICANT: Li, Guihua
; TITLE OF INVENTION: Sunflower Disease Resistance Genes
; FILE REFERENCE: 35718/200630
; CURRENT APPLICATION NUMBER: US/09/602,472A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/140,876
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2114
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2114)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1475
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1475
; OTHER INFORMATION: n = A,T,C or G
US-09-602-472A-5

Alignment Scores:

Pred. No.:	2.96e-16	Length:	2114
Score:	578.00	Matches:	143
Percent Similarity:	55.07%	Conservative:	85
Best Local Similarity:	34.54%	Mismatches:	136
Query Match:	16.74%	Indels:	51
DB:	4	Gaps:	15

US-10-086-464-2 (1-647) x US-09-602-472A-5 (1-2114)

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Qy        235 SerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerProGlyLeu 254
Db         52 GCTGAATCTTCCTCCTCATATTCACCACAACCGTGC----------------------- 87

Qy        255 ValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGly 274
Db         88 ------------------CGTCAATTTACCTTTTCGGAGATTCAACTTGCAACCCAAAAC 129

Qy        275 PheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeu 294
Db        130 TTTGATGAGTCGTTGGTGATAGGACGTGGGGGGTTTGGCAAGGTTTACAGAGGAACCTTC 189

Qy        295 ProSerGlyLys---------GluValAlaValLysGlnLeuLysValGlySerGlyGln 311
Db        190 ACTTATGGGGAAACATACTTGGATGCTGCAATTAAGCGACTGGAATCAGGTTCTAGTCAA 249

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331
Db        250 GGAGCGGTAGAGTTTAGGGCTGAAATTGAGATGCTCTCAAATCTAAGGCACTGTCATTTG 309

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351
Db        310 GTGTCTTTAATTGGTTACTGTAGTGATGGGCAAGAGATGGTTCTTGTATATGAACATATG 369

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371
Db        370 CCCAATGGAACTCTTGCAGATCGTCTCCAC---AAGCGTCGAGCTCCTCTAACTTGGGTA 426

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis------Glu 389
Db        427 AGAAGACTCAAAATATGCATAGGGGCCGCTCGTGGTTTAGATTACTTGCACACTGGTACG 486

Qy        390 AspCysAsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPhe 409
Db        487 GGTATTAACCATGGAGTTATACATCGGGATGTTAAGAGCACAAATATATTGTTAGATGAC 546

Qy        410 LysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIle------AlaSerAspThr 427
Db        547 AATTGGGCAGCTAAGGTTTCTGACTTTGGTTTGTCCAAAATTGGTCCAACAAATCAGCCT 606

Qy        428 AsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Qy        448 AlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGlu 467
Db        667 CAAACAGGTAGGCTGACTCGAAAGTCTGACGTGTATGCCTTTGGGGTGGTCCTGTTTGAA 726

Qy        468 LeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuVal 487
Db        727 GTCCTATGTGGGAAACAAGTAGTACTGATGAGGAGCAC-TGG---------GGTTTGGCA 776

Qy        488 AspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAla 507
Db        777 ACATGGGCTCAAGACTCTCTT-----------AAAGAAGGAAGGCTAAAGCAAATTGTT 824

Qy        508 AspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAla 527
Db        825 GATTCTAATTTAAGGGGGAGAATATCCCCAAAATGTTTGAAGGAGTTTGCACTACTAGCT 884

Qy        528 AlaAlaCysValArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAla 547
Db        885 GACCGGTGTTTGCATAGCCGTCCCAAGCAACGTCCTGCAATGGCGGAGGTTGTGATTGGT 944

Qy        548 LeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly-----------------Met 561
Db        945 CTTGAGTCAATCCTAGCCTTACAGGAGAAAACCGAGAGTACATGGGTACCAACATTTCTC 1004

Qy        562 ArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSer 581
Db       1005 TTTCCA---------TCCACTTGGGAAAAGACAGTTGGAGGTACAGATTTAAAATCCCTG 1055

Qy        582 Gln---------TyrAsn---------GluAsp------MetLysLysPheArgLysMet 593
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Qy        612 AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGln 625
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RESULT 15
US-08-265-628-1
; Sequence 1, Application US/08265628
; Patent No. 5821094
;  GENERAL INFORMATION:
;    APPLICANT:  Rothstein, Steven J.
;    APPLICANT:  Goring, Daphne
;    TITLE OF INVENTION:  S-LOCUS RECEPTOR KINASE GENE IN A
;    TITLE OF INVENTION:  SELF-INCOMPATIBLE BRASSICA NAPUS LINE
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 W. Madison St.   Suite 3400
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,628
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/959,945
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/847,564
;      FILING DATE:  03-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pochopien Ph.D., Donald J.
;      REGISTRATION NUMBER:  32,167
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-707-8889
;      TELEFAX:  312-707-9155
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2749 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Brassica napus
;      STRAIN:  oleifera
;      INDIVIDUAL ISOLATE:  W1
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  S-locus
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2574
;    PUBLICATION INFORMATION:
;      AUTHORS:  GORING, DAPHNE
;      AUTHORS:  ROTHSTEIN, STEVEN J.
;      TITLE:  THE S-LOCUS RECEPTOR KINASE GENE IN A
;      TITLE:  SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES A
;      TITLE:  FUNCTIONAL SERINE/THREONINE KINASE
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 2749
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US-08-265-628-1

Alignment Scores:

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Percent Similarity:	49.80%	Conservative:	94
Best Local Similarity:	30.92%	Mismatches:	160
Query Match:	16.65%	Indels:	91
DB:	1	Gaps:	14

US-10-086-464-2 (1-647) x US-08-265-628-1 (1-2749)

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Db       1810 TATTTAGAAAATTTAAGCCTCGATTCTTATCTCTTCGGAAATAAACGAAGCTCTACGTTA 1869

Qy        369 GluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHis 388
                |||      |||      |||      |||   |||:::||||||   |||||||||
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Qy        409 PheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsn 428
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Qy        429 ThrHisValSerThrArg---ValMetGlyThrPheGlyTyrLeuAlaProGluTyrAla 447
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Search completed: May 13, 2004, 01:36:26
Job time : 187 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 13, 2004, 00:33:06 ; Search time 677 Seconds
(without alignments)
4329.253 Million cell updates/sec

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Perfect score: 3453
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_p/US10086464/runat_11052004_121817_7949/app_query.fasta_1.839
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN=2000000000 -USER=US10086464_@CGN_1_1_333_@runat_11052004_121817_7949
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14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	3453	100.0	2189	14	US-10-086-464-3	Sequence 3, Appli
3	2285.5	66.2	2451	13	US-10-424-599-95479	Sequence 95479, A
4	1870	54.2	1724	13	US-10-425-114-2326	Sequence 2326, Ap
5	1833	53.1	2880	13	US-10-425-114-33030	Sequence 33030, A
6	1833	53.1	2881	13	US-10-425-114-33031	Sequence 33031, A
7	1748.5	50.6	1902	14	US-10-086-464-10	Sequence 10, Appl
8	1748.5	50.6	1939	14	US-10-086-464-9	Sequence 9, Appli
9	1737.5	50.3	1424	13	US-10-425-114-9117	Sequence 9117, Ap
10	1687	48.9	2025	14	US-10-086-464-13	Sequence 13, Appl
11	1687	48.9	2104	14	US-10-086-464-12	Sequence 12, Appl
12	1539	44.6	2655	13	US-10-424-599-57846	Sequence 57846, A
13	1539	44.6	2655	13	US-10-425-114-7339	Sequence 7339, Ap
14	1437.5	41.6	2190	13	US-10-425-114-14127	Sequence 14127, A
15	1437	41.6	1500	13	US-10-425-114-6300	Sequence 6300, Ap
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17	1415.5	41.0	2196	14	US-10-086-464-7	Sequence 7, Appli
18	1415.5	41.0	2231	14	US-10-086-464-6	Sequence 6, Appli
19	1400.5	40.6	2261	14	US-10-086-464-15	Sequence 15, Appl
20	1399	40.5	2196	14	US-10-086-464-16	Sequence 16, Appl
21	1379	39.9	2508	13	US-10-425-114-25269	Sequence 25269, A
22	1335.5	38.7	1585	13	US-10-424-599-71008	Sequence 71008, A
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24	1238.5	35.9	1462	13	US-10-425-114-29328	Sequence 29328, A
25	1233.5	35.7	1134	13	US-10-425-114-36420	Sequence 36420, A
26	1210	35.0	1795	13	US-10-424-599-42232	Sequence 42232, A
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28	1116.5	32.3	1186	13	US-10-425-114-4273	Sequence 4273, Ap
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30	921	26.7	729	13	US-10-425-114-12191	Sequence 12191, A
31	892.5	25.8	760	13	US-10-425-114-12314	Sequence 12314, A
32	866.5	25.1	951	13	US-10-425-114-1922	Sequence 1922, Ap
33	860.5	24.9	1777	13	US-10-425-114-24475	Sequence 24475, A
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35	840	24.3	2025	13	US-10-425-114-3666	Sequence 3666, Ap
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38	825	23.9	2012	13	US-10-424-599-29210	Sequence 29210, A
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40	816.5	23.6	2124	9	US-09-938-842A-1079	Sequence 1079, Ap
41	816.5	23.6	2124	11	US-09-938-842A-1079	Sequence 1079, Ap
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43	806.5	23.4	2063	13	US-10-424-599-25617	Sequence 25617, A
44	804	23.3	2374	13	US-10-425-114-33063	Sequence 33063, A
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ALIGNMENTS

RESULT 1
US-10-086-464-1
; Sequence 1, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1944
; TYPE: DNA

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;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1944)
US-10-086-464-1

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Pred. No.:              9.36e-216       Length:         1944
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x US-10-086-464-1 (1-1944)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660

Qy        221 ProArgGlnProProProProProProProProPheMetSerSerSerGlyGlySerAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy        641 GlyTyrSerGlyProSerLeu 647
              |||||||||||||||||||||
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Db       1921 GGTTATAGTGGACCTTCTCTT 1941

RESULT 2
US-10-086-464-3
; Sequence 3, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2189
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2189)
;   OTHER INFORMATION:
US-10-086-464-3

Alignment Scores:
Pred. No.:              1.05e-215       Length:         2189
Score:                  3453.00         Matches:        647
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     14              Gaps:           0

US-10-086-464-2 (1-647) x US-10-086-464-3 (1-2189)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThr 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 156

Qy         21 ThrThrThrProProProAlaSerAlaProProProThrThrProSerSerProProPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy         41 ProSerThrIleProThrSerProProProSerSerArgSerThrProSerAlaProPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 276

Qy         61 ProSerProProThrProSerThrProGlySerProProProLeuProGlnProSerPro 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 336

Qy         81 ProAlaProThrThrProGlySerProProAlaProValThrProProThrArgAsnPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        101 ProProSerValProGlyProProSerAsnProSerArgGluGlyGlySerProArgPro 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        121 ProSerSerProSerProProSerProSerSerAspGlyLeuSerThrGlyValValVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        141 GlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCys 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy        161 LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProProProProProPro 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        181 GlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        201 ThrProProSerAspHisValValThrSerLeuProProProProLysAlaProSerPro 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        221 ProArgGlnProProProProProProProProProMetSerSerSerGlyGlySerAsp 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        241 TyrSerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLys 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        261 SerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeu 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        281 LeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        301 AlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluVal 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        321 GluIleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAla 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy        341 GlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy        361 HisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy        381 AlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIle 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy        401 LysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeu 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy        421 AlaLysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy        441 TyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSer 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy        461 PheGlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnVal 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy        481 TyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGln 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy        501 GlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMet 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656
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Qy        521 AlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArg 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy        541 MetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGly 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy        561 MetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSer 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy        581 SerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyr 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy        601 AsnAlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySer 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy        621 SerSerGluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGlyGln 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy        641 GlyTyrSerGlyProSerLeu 647
              |||||||||||||||||||||
Db       2017 GGTTATAGTGGACCTTCTCTT 2037

RESULT 3
US-10-424-599-95479
; Sequence 95479, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 95479
;   LENGTH: 2451
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_57229C.1
US-10-424-599-95479

Alignment Scores:
Pred. No.:              9.23e-140      Length:          2451
Score:                  2285.50        Matches:         450
Percent Similarity:     80.86%         Conservative:    74
Best Local Similarity:  69.44%         Mismatches:      97
Query Match:            66.19%         Indels:          27
DB:                     13             Gaps:            16

US-10-086-464-2 (1-647) x US-10-424-599-95479 (1-2451)

Qy         13 ProSerProProProSerAsnSerThrThrThrThrProProProAla------SerAlaPro 30
              |||   ||||||      :::|||   ::::::||||||||||||      |||:::|||
Db        246 CCCCTCCCTCCGCCT---GCAACTCCGTCGTCACCTCCGCCGGCAACTCCGTCGTCTCCT 302

Qy         31 ProProThrThrProSerSerProProProProSerThrIleProThrSerProProPro 50
              ||||||   ||||||||||||||||||||      :::   |||:::|||||||||||||
Db        303 CCGCCGGCGACACCTTCTTCGCCACCTCCG------TCAACTCCTTCCTCGCCCCCTCCG 356

Qy         51 SerSerArgSerThrProSerAlaProProProSerProProThrProSerThrProGly 70
                    :::||||||||||||   |||||||||   |||:::   |||   |||
Db        357 ---------GCGACTCCCTCCGCTTCTCCACCGTCCACTCCTTCTGCTTCTCCTCCACCG 407

Qy         71 SerProProProLeuProGlnProSerProProAlaProThrThrProGlySerProPro 90
              |||   |||       |||       |||||||||:::   |||:::|||   |||||||||
Db        408 TCCACTCCAACCACGCCGTCAACTTCGCCGCCATCG---ACTTCTCCGCCGTCGCCGCCA 464

Qy         91 ------AlaProValThrProProThrArgAsnProProProSerValProGlyProPro 108
                    :::|||   :::|||||:::                 |||   |||   ||||||
Db        465 TCGCACTCGCCGCCGTCGCCTCCCAGTGGCGGCGGAGGCGGCAGCACTCCGAGTCCACCG 524

Qy        109 SerAsnProSerArgGluGlyGlySerProArgProProSerSerProSerProProSer 128
              |||       |||             |||         |||:::::|||||||||||||||||
Db        525 TCCCGGAGCTCGCCCTCTCCTCCGTCCGGATCGAGACCGACCACTCCGTCGCCTCCGTCG 584

Qy        129 ProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGlyGlyValAla 148
                  ||||||      :::|||||||||||||||||||||||||||:::|||   ||||||
Db        585 TCTTCCTCGTCGAGTATTTCGACCGGTGTGGTGGTGGGAATCGCCGTTGGGGCTGTGGCG 644

Qy        149 LeuLeuValIleValThrLeuIleCysLeuLeuCys---LysLysLysArgArgArgAsp 167
              :::|||::::::::::::::::::|||:::   |||   ||||||||||||||||||||
Db        645 GTTCTTCTTGTGTTGAGCATTCTCTGCATATGTTGCCGGAAGAAGAAGAGAAGACGTGAT 704

Qy        168 GluGluAspAlaTyrTyrValProProProProProPro---GlyProLysAlaGlyGly 186
              ||||||      ||||||   |||||||||   ||||||   |||||||||
Db        705 GAAGAG------TACTATGCTCCGCCGCCGCAACCGCCGCGGGGACCTAAA---GATGAT 755

Qy        187 ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHis 206
                  |||||||||      :::||||||   |||   |||      ||||||   ||||||
Db        756 GCATATGGTGGTCCCCCACGTCAATGG---CAACACAATGTTCCCCCTCCTCAAGATCAT 812

Qy        207 ValValThrSerLeuProPro---------ProProLysAlaProSerProProArgGln 223
              ||||||:::   :::||||||         ||||||   ||||||
Db        813 GTGGTCTCAATGATGCCTCCAAAGCCATCGCCACCACCTGCTCCACCGGCTTATGCTGGT 872

Qy        224 ProProProProProProProProPheMetSerSerSerGly------GlySerAspTyr 241
                  ||||||||||||||||||||||:::|||||||||||||      ||||||:::|||
Db        873 CAACCTCCCCCACCACCGCCTCCTTTCATCAGCAGCAGTGGCGGATCTGGATCAAACTAT 932

Qy        242 SerAspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSer 261
              |||         ||||||||||||||||||||:::   ||||||||||||||||||
Db        933 TCAGGCGGTGAATTTCTTCCTCCTCCTTCTCCAGGAATTTCATTGGGATTCTCTAAGAGC 992

Qy        262 ThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeu 281
              ||||||||||||||||||||||||||||||||||:::|||||||||:::||||||||||||
Db        993 ACATTCACGTATGAGGAGTTGGCACGCGCAACTGATGGCTTCTCTGATGCCAACCTCCTT 1052

Qy        282 GlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAla 301
              ||||||||||||||||||||||||||:::|||:::||||||:::||||||||||||||||
Db       1053 GGACAAGGAGGATTTGGATATGTGCACAGAGGAATTCTTCCCAACGGCAAGGAGGTGGCA 1112

Qy        302 ValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGlu 321
              ||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1113 GTGAAGCAATTGAAGGCTGGAAGCGGGCAAGGGGAGCGTGAATTCCAAGCTGAAGTTGAG 1172

Qy        322 IleIleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGly 341
              ||||||||||||||||||||:::|||||||||||||||||||||||||||||||   |||
Db       1173 ATAATTAGCCGTGTCCATCACAAGCATCTTGTTTCTTTGGTTGGATACTGCATCACTGGG 1232

Qy        342 AlaLysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHis 361
              ::::::|||||||||||||||||||||||||||||||   ||||||   |||||||||
Db       1233 TCCCAGAGGCTGCTTGTTTATGAATTTGTTCCCAACAACACATTGGAATTCCATTTGCAT 1292

Qy        362 GlyGluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAla 381
              |||:::|||||||||||||||:::|||   |||||||||:::|||||||||||||||||||
Db       1293 GGAAAAGGGCGACCTACCATGGATTGGCCCACAAGACTAAGAATTGCTTTAGGATCTGCT 1352

Qy        382 LysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLys 401
              |||||||||:::|||||||||||||||||||:::|||||||||||||||||||||||||||
Db       1353 AAGGGACTGGCGTATCTTCATGAAGATTGTCATCCTAAGATCATCCATCGTGATATCAAA 1412

Qy        402 AlaSerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAla 421
              |||:::|||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCTGCCAACATCCTTCTGGATTTTAAGTTTGAAGCAAAGGTTGCAGATTTTGGTCTTGCA 1472

Qy        422 LysIleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyr 441
```

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Db       1473 AAGTTTTCTTCTGATGTCAATACCCATGTTTCTACTCGAGTGATGGGGACTTTTGGGTAT 1532

Qy        442 LeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPhe 461

Db       1533 TTGGCTCCAGAATATGCTTCTAGTGGAAAACTGACAGACAAATCAGATGTTTTCTCCTAT 1592

Qy        462 GlyValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyr 481

Db       1593 GGAGTCATGCTCCTCGAGTTAATAACCGGACGACGGCCAGTCGATAAAAATCAAACTTTC 1652

Qy        482 ValAspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGly 501

Db       1653 ATGGAGGATAGTTTGGTAGACTGGGCTAGGCCTTTGCTCACACGAGCTTTGGAAGAGGAT 1712

Qy        502 AspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAla 521

Db       1713 GATTTTGATTCTATTATTGACCCAAGGCTCCAGAATGACTATGATCCTAATGAGATGGCA 1772

Qy        522 ArgMetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMet 541

Db       1773 CGAATGGTGGCTTCTGCTGCGGCTTGCATTCGTCATTCGGCAAAGCGTCGACCAAGGATG 1832

Qy        542 SerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMet 561

Db       1833 AGCCAGGTTGTTCGCGCTCTGGAAGGAGATGTCTCTCTAGCAGATCTTAACGAAGGAATT 1892

Qy        562 ArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSer 581

Db       1893 AGACCTGGACACAGCACTATGTACAGTTCTCAT---GAAAGCTCAGATTATGACACTGCA 1949

Qy        582 GlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsn 601

Db       1950 CAGTACAAGGAAGACATGAAAAAGTTCAGAAAAATGGCATTGGGAACTCAGGAGTATGGT 2009

Qy        602 AlaThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSer 621

Db       2010 GCAAGCAGTGAGTACAGTGCCGCTACAAGTGAGTATGGTTTAAACCCATCAGGCTCAAGT 2069

Qy        622 SerGluGly---------GlnThrThrArgGluMetGluMetGlyLysIleLysArgThr 638

Db       2070 AGTGAAGCACAGAGCCGCCAAACCACAAGGGAAATGGAAATGAGAAAGATGAAG---AAC 2126

Qy        639 GlyGlnGlyTyrSerGlyProSer 646

Db       2127 AATCAAGGTTTCAGTGGAAGTTCT 2150

RESULT 4
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
;   LENGTH: 1724
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

Alignment Scores:

Pred. No.:              6.76e-113      Length:          1724
Score:                  1870.00        Matches:         363
Percent Similarity:     79.85%         Conservative:    53
Best Local Similarity:  69.67%         Mismatches:      87
Query Match:            54.16%         Indels:          18
DB:                     13             Gaps:            9

US-10-086-464-2 (1-647) x US-10-425-114-2326 (1-1724)

Qy        139 ValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIleValThrLeuIleCysLeu 158

Db          1 GTCGTGGGCGTGGCCGTCGGCGGCCTCGTGCTGCTGCTGCTCGCCAGCTTCATCTGCCTC 60

Qy        159 LeuCys------LysLysLysArgArgArgAspGluGluAspAlaTyrTyrValProPro 176

Db         61 TGCTGTCTCCGCAAGAAGCGCCGCCGCGCGCCGCCGCCGCCTCAGCACTACGGATACCCG 120

Qy        177 ProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGlnGlnGlnTrpArg 196

Db        121 CCGCCCCCGCCG---CCGTACAAGGAGGATCCATACGGTGGAACGTACCAGAGTTGG--- 174

Qy        197 GlnGlnAsnAla------ThrProProSerAspHisValValThrSerLeuPro---Pro 213

Db        175 CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAACATGTGGTCAAGATGCACCCTTCGCCT 234

Qy        214 ProProLysAlaProSerProProArgGlnProProProProProProProProPheMet 233

Db        235 CCGCCAGCATATGCCAATCGTCCTCCACAGCCGCCAGCGCCGCCACCACCAGCGATGCTA 294

Qy        234 SerSerSerGly------GlySerAspTyrSerAspArgProValLeuProProProSer 251

Db        295 AATAGTAGTGGTGGATCTGGTTCTAATTACTCTGGTGGCGAGATCCTACCTCCACCATCC 354

Qy        252 ProGlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAla 271

Db        355 CCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACATTCACCTACGAAGAGTTGTTGAGGGCT 414

Qy        272 ThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLys 291

Db        415 ACTGATGGATTCTCGGATGCTAATCTCCTTGGACAAGGTGGTTTTGGCTATGTTCACAGA 474

Qy        292 GlyValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGln 311

Db        475 GGATTGCTGCCTAATGGCAAAGAGATTGCTGTAAAACAACTGAAACTGGGAAGTGGCCAG 534

Qy        312 GlyGluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeu 331

Db        535 GGCGAGCGTGAGTTCCAGGCTGAGGTTGAGATTATCAGCCGAGTACATCACAAACACCTT 594

Qy        332 ValSerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheVal 351

Db        595 GTGTCTTTGGTTGGCTATTGCATTTCTGGAGGCAAGAGGCTGCTTGTCTATGAGTTTGTC 654

Qy        352 ProAsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSer 371

Db        655 CCCAATAACACATTGGAATTCCACTTACATGCGAAAGATCGACCAACAATGGAGTGGCCT 714

Qy        372 ThrArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCys 391

Db        715 GCTAGATTAAAGATCAGTTTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGC 774

Qy        392 AsnProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPhe 411

Db        775 CATCCAAAGATCATCCATCGTGACATAAAGGCATCTAACATTCTTCTTGACTTCCAATTT 834

Qy        412 GluAlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisVal 431

Db        835 GAAGCTAAGGTTGCTGATTTTGGACTTGCAAAGTTCACTACTGATAACAACACCCATGTT 894

Qy        432 SerThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLys 451

Db        895 TCGACAAGAGTAATGGGCACCTTTGGGTATTTGGCACCTGAGTATGCATCTTCTGGCAAG 954
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Qy        452 LeuThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGly 471
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        955 CTAACAGAAAAATCTGATGTATTTTCCTTCGGAGTCATGCTTCTTGAGCTTATTACTGGG 1014

Qy        472 ArgArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArg 491
              ||||||||||||||||           |||:::||||||||||||||||||||||||||
Db       1015 CGGCGACCAGTTGACACAACCCAAACATATATGGATGACAGCTTGGTTGACTGGGCAAGG 1074

Qy        492 ProLeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMet 511
              |||||||||   ||||||   |||   |||:::::::::   |||   |||    ::::::
Db       1075 CCATTACTGATGCGAGCACTTGAGGATGGTGAATATGATGCTTTAGTGGATCCTCGGCTG 1134

Qy        512 AsnAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysVal 531
                    ::::::     ||||||||||||||||:::||||||||||||||||||||
Db       1135 GGAAAGGACTTCAATCCTAATGAGATGGCAAGAATGATAGCCTGTGCAGCTGCATGTGTA 1194

Qy        532 ArgHisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsn 551
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       1195 CGCCATTCTGCACGTCGTCGGCCACGTATGAGTCAGGTTGTTCGGGCTTTGGAGGGCAAT 1254

Qy        552 ValSerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSer 571
              |||||||||   ||||||||||||||:::|||||||||   |||      :::   |||
Db       1255 GTGTCTTTGGAGGACCTTAATGAAGGTGTTCGGCCTGGCCATAGCCGCTTCTTTGGGTCA 1314

Qy        572 TyrGlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArg 591
              |||      |||:::||||||||||||   ||||||||||||||||||||||||||:::
Db       1315 TAC---AGCAGCTCCGATTACGATTCTGGCCAGTACAACGAGGACATGAAGAAGTTCAAG 1371

Qy        592 LysMetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSer 611
              |||||||||                              :::   :::||||||   |||||||||
Db       1372 AAGATGGCATTCAACAACAAC------TATACCAGCAGCCAATACAGCGCGCCAACCAGT 1425

Qy        612 AspTyrGlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGlu 631
              :::||||||      ||||||   ||||||||||||||      |||:::|||||||||
Db       1426 GAATATGGACAGATACCGTCTGCATCAAGCAGCGAGGGCCACCAGACGCAGGAGATGGAG 1485

Qy        632 MetGlyLysIleLysArgThrGly-----------------GlnGlyTyrSerGlyPro 645
                 |||   :::|||:::   |||                ||||||||||
Db       1486 TCGGGTGCAATGAAGAAAGGTGGCTACAGTGGTGGCTACAGCTCAGGATACAGCGGAGCC 1545

Qy        646 Ser 646
              |||
Db       1546 TCG 1548
```

RESULT 5
US-10-425-114-33030
; Sequence 33030, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33030
;   LENGTH: 2880
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B11_FLI
US-10-425-114-33030

Alignment Scores:

Pred. No.:	2.81e-110	Length:	2880
Score:	1833.00	Matches:	356
Percent Similarity:	79.80%	Conservative:	51
Best Local Similarity:	69.80%	Mismatches:	85
Query Match:	53.08%	Indels:	18
DB:	13	Gaps:	9

US-10-086-464-2 (1-647) x US-10-425-114-33030 (1-2880)

```
Qy        150 LeuValIleValThrLeuIleCysLeuLeuCys------LysLysLysArgArgArgAsp 167
              :::::::::   :::   |||||||||   |||      ||||||:::||||||
Db       1138 GTGCTGCTCGCCAGCTTCATCTGCCTCTGCTGTCTCCGCAAGAAGCGCCGCCGCGCCG 1197

Qy        168 GluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGlyGlyPro 187
                       :::|||      ||||||||||||||   |||            |||
Db       1198 CCGCCGCCTCAGCACTACGGATACCCGCCGCCCCCGCCG---CCGTACAAGGAGGATCCA 1254

Qy        188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla------ThrProProSerAsp 205
              |||||||||      |||   |||   ||||||||||||         ||||||   :::
Db       1255 TATGGTGGAACGTACCAGAGTTGG---CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAA 1311

Qy        206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGlnPro 224
              |||||||||          |||   |||||||||          :::   |||   ||||||
Db       1312 CATGTGGTCAAGATGCACCCTTCGCCTCCGCCAGCATATGCCAATCGTCCTCCACAGCCG 1371

Qy        225 ProProProProProProProPheMetSerSerSerGly------GlySerAspTyrSer 242
              |||   ||||||||||||      ::::::||||||||      |||||||:::||||||
Db       1372 CCAGCGCCGCCACCACCAGCGATGCTAAATAGTAGTGGTGGATCTGGTTCTAATTACTCT 1431

Qy        243 AspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThr 262
                  :::||||||||||||||||||||||   ||||||||||||||||||||||||
Db       1432 GGTGGCGAGATCCTACCTCCACCATCCCCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACA 1491

Qy        263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGly 282
              ||||||||||||||||||   |||||||||:::|||||||||:::|||||||||||||||
Db       1492 TTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCTAATCTCCTTGGA 1551

Qy        283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
              ||||||||||||||||||||||||||:::|||:::|||||||:::||||||||:::|||||
Db       1552 CAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAAGAGATTGCTGTA 1611

Qy        303 LysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIle 322
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db       1612 AAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCTGAGGTTGAGATT 1671

Qy        323 IleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
              ||||||||||||||||||:::|||||||||||||||||||||||||||||:::|||
Db       1672 ATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGCATTTCTGGAGGC 1731

Qy        343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGly 362
              ||||||||||||||||||||||||||||||||||||||||||   ||||||   |||||||||
Db       1732 AAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTCCACTTACATGCG 1791

Qy        363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
              :::|||||||||||||||||||||      ||||||||||:::|||||:::||||||
Db       1792 AAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTGGGTGCTGCCAAG 1851

Qy        383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
              ||||||:::|||||||||||||||||||:::||||||||||||||||||||||||||||
Db       1852 GGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCA 1911

Qy        403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
              ||||||||||||:::||||||:::||||||||||||||||||||||||||||||||||||
Db       1912 TCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGACTTTGGACTTGCAAAG 1971

Qy        423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
                    :::|||   ||||||||||||||||||||||||||||||||||||||||||||
Db       1972 TTCACTACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTG 2031

Qy        443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db       2032 GCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGA 2091

Qy        463 ValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrVal 482
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||:::
Db       2092 GTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATG 2151
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```
Qy        483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db       2152 GATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAA 2211

Qy        503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
Db       2212 TATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGA 2271

Qy        523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSer 542
Db       2272 ATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGT 2331

Qy        543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562
Db       2332 CAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGG 2391

Qy        563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582
Db       2392 CCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAG 2448

Qy        583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602
Db       2449 TACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACC 2502

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622
Db       2503 AGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGC 2562

Qy        623 GluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly--------- 639
Db       2563 GAGGGCCACCAGACGCAGGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGT 2622

Qy        640 ---------GlnGlyTyrSerGlyProSer 646
Db       2623 GGCTACAGCTCAGGATACAGCGGAGCCTCG 2652

RESULT 6
US-10-425-114-33031
; Sequence 33031, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33031
;   LENGTH: 2881
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17055B12_FLI
US-10-425-114-33031

Alignment Scores:
Pred. No.:              2.81e-110      Length:         2881
Score:                  1833.00        Matches:        356
Percent Similarity:     79.80%         Conservative:   51
Best Local Similarity:  69.80%         Mismatches:     85
Query Match:            53.08%         Indels:         18
DB:                     13             Gaps:           9

US-10-086-464-2 (1-647) x US-10-425-114-33031 (1-2881)

Qy        150 LeuValIleValThrLeuIleCysLeuLeuCys------LysLysLysArgArgArgAsp 167

Db       1139 GTGCTGCTCGCCAGCTTCATCTGCCTCTGCTGTCTCCGCAAGAAGCGCCGCCGCGCCG 1198

Qy        168 GluGluAspAlaTyrTyrValProProProProProGlyProLysAlaGlyGlyPro 187
Db       1199 CCGCCGCCTCAGCACTACGGATACCCGCCGCCCCCGCCG---CCGTACAAGGAGGATCCA 1255

Qy        188 TyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAla------ThrProProSerAsp 205
Db       1256 TATGGTGGAACGTACCAGAGTTGG---CAGCAAAATGCGCCTCCTGCTCCACCCCCTGAA 1312

Qy        206 HisValValThrSerLeuPro---ProProProLysAlaProSerProProArgGlnPro 224
Db       1313 CATGTGGTCAAGATGCACCCTTCGCCTCCGCCAGCATATGCCAATCGTCCTCCACAGCCG 1372

Qy        225 ProProProProProProProPheMetSerSerSerGly------GlySerAspTyrSer 242
Db       1373 CCAGCGCCGCCACCACCAGCGATGCTAAATAGTAGTGGTGGATCTGGTTCTAATTACTCT 1432

Qy        243 AspArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThr 262
Db       1433 GGTGGCGAGATCCTACCTCCACCATCCCCTGGTGCTGTTCTTGGCTTCTCGAAGAGCACA 1492

Qy        263 PheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGly 282
Db       1493 TTCACCTACGAAGAGCTGTTGAGGGCTACTGATGGATTCTCGGATGCTAATCTCCTTGGA 1552

Qy        283 GlnGlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaVal 302
Db       1553 CAAGGTGGTTTTGGCTATGTTCACAGAGGATTGCTGCCTAATGGCAAAGAGATTGCTGTA 1612

Qy        303 LysGlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIle 322
Db       1613 AAACAATTGAAACTGGGAAGTGGCCAGGGAGAGCGTGAGTTCCAGGCTGAGGTTGAGATT 1672

Qy        323 IleSerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAla 342
Db       1673 ATCAGCCGAGTACATCACAAACACCTTGTGTCTTTGGTTGGCTATTGCATTTCTGGAGGC 1732

Qy        343 LysArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGly 362
Db       1733 AAGAGGCTGCTTGTCTATGAGTTTGTCCCCAATAACACATTGGAATTCCACTTACATGCG 1792

Qy        363 GluGlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLys 382
Db       1793 AAAGGTCGACCAACAATGGAGTGGCCTGCTAGATTAAAGATCAGTTTGGGTGCTGCCAAG 1852

Qy        383 GlyLeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAla 402
Db       1853 GGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGATCATCCATCGTGACATAAAGGCA 1912

Qy        403 SerAsnIleLeuIleAspPheLysPheGluAlaLysValAlaAspPheGlyLeuAlaLys 422
Db       1913 TCTAACATTCTTCTTGACTTCCAATTTGAAGCTAAGGTTGCTGACTTTGGACTTGCAAAG 1972

Qy        423 IleAlaSerAspThrAsnThrHisValSerThrArgValMetGlyThrPheGlyTyrLeu 442
Db       1973 TTCACTACTGATAACAACACCCATGTTTCGACAAGAGTAATGGGCACCTTTGGGTATTTG 2032

Qy        443 AlaProGluTyrAlaAlaSerGlyLysLeuThrGluLysSerAspValPheSerPheGly 462
Db       2033 GCACCTGAGTATGCATCTTCTGGCAAGCTAACAGAAAAATCCGATGTATTTTCCTTCGGA 2092

Qy        463 ValValLeuLeuGluLeuIleThrGlyArgArgProValAspAlaAsnAsnValTyrVal 482
Db       2093 GTCATGCTTCTTGAGCTTATTACTGGGCGGCGACCAGTTGACACAACCCAAACATATATG 2152

Qy        483 AspAspSerLeuValAspTrpAlaArgProLeuLeuAsnArgAlaSerGluGlnGlyAsp 502
Db       2153 GATGACAGCTTGGTTGACTGGGCAAGGCCATTACTGATGCGAGCACTTGAGGATGGTGAA 2212

Qy        503 PheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTyrAspArgGluGluMetAlaArg 522
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Db       2213 TATGATGCTTTAGTGGATCCTCGGCTGGGAAAGGACTTCAATCCTAATGAGATGGCAAGA 2272

Qy        523 MetValAlaCysAlaAlaAlaCysValArgHisSerAlaArgArgArgProArgMetSer 542

Db       2273 ATGATAGCCTGTGCAGCTGCATGTGTACGCCATTCTGCACGTCGTCGGCCACGTATGAGT 2332

Qy        543 GlnIleValArgAlaLeuGluGlyAsnValSerLeuSerAspLeuAsnGluGlyMetArg 562

Db       2333 CAGGTCGTTCGGGCTTTGGAGGGCAATGTGTCTTTGGAGGACCTTAATGAAGGTGTTCGG 2392

Qy        563 ProGlyGlnSerAsnValTyrSerSerTyrGlyGlySerThrAspTyrAspSerSerGln 582

Db       2393 CCTGGCCATAGCCGCTTCTTTGGGTCATAC---AGCAGCTCCGATTACGATTCTGGCCAG 2449

Qy        583 TyrAsnGluAspMetLysLysPheArgLysMetAlaLeuGlyThrGlnGluTyrAsnAla 602

Db       2450 TACAACGAGGACATGAAGAAGTTCAAGAAGATGGCATTCAACAACAAC------TATACC 2503

Qy        603 ThrGlyGluTyrSerAsnProThrSerAspTyrGlyLeuTyrProSerGlySerSerSer 622

Db       2504 AGCAGCCAATACAGCGCGCCAACCAGTGAATATGGACAGATACCGTCTGCATCAAGCAGC 2563

Qy        623 GluGlyGlnThrThrArgGluMetGluMetGlyLysIleLysArgThrGly--------- 639

Db       2564 GAGGGCCACCAGACGCAGGAGATGGAGTCGGGTGCAATGAAGAAAGGTGGCTACAGTGGT 2623

Qy        640 ---------GlnGlyTyrSerGlyProSer 646

Db       2624 GGCTACAGCTCAGGATACAGCGGAGCCTCG 2653

RESULT 7
US-10-086-464-10
; Sequence 10, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1902
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1902)
US-10-086-464-10

Alignment Scores:
Pred. No.:              5.88e-105      Length:          1902
Score:                  1748.50        Matches:          367
Percent Similarity:     69.67%         Conservative:      81
Best Local Similarity:  57.08%         Mismatches:       141
Query Match:            50.64%         Indels:            55
DB:                     14             Gaps:              16

US-10-086-464-2 (1-647) x US-10-086-464-10 (1-1902)

Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22

Db         19 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 78

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42

Db         79 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 129

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62

Db        130 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 189

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82

Db        190 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 246

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102

Db        247 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 306

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120

Db        307 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 357

Qy        121 ProSer------------------SerProSerProProSerPro------SerSerAsp 132

Db        358 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 417

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        418 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 477

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165

Db        478 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 537

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGly 185

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Qy        186 GlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp 205

Db        568 AACCAATAT---------CAATACTA-TGGAAACAACAACAACAACAATGCTTCACAGAA 617

Qy        206 HisValValThrSerLeuProProProProLysAlaProSerProPro------------ 221

Db        618 ------TTATCCGAATTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGG 671

Qy        222 ------ArgGln-ProProProProProProProProPheMetSerSerSerGly----- 237

Db        672 TTGGGGAGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGA 731

Qy        238 -GlySerAspTyrSer------AspArgProValLeuProProProSerProGlyLeuVa 255

Db        732 TTCTTCCATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGC 791

Qy        255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275

Db        792 CCTCGGATTCAACAAGAGCACTTTTACTTACCAAGAGCTTGCGGCTGCAACAGGAGGGTT 851

Qy        275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295

Db        852 TACGGATGCTAACCTTTTGGGACAGGGAGGATTTGGGTATGTCCATAAAGGAGTCTTGCC 911

Qy        295 oSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluArgGl 315

Db        912 TAGCGGGAAAGAAGTAGCAGTTAAGAGTTTAAAAGCGGGTAGCGGACAAGGAGAGAGGGA 971

Qy        315 uPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuValSerLeuVa 335

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Qy        335 lGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAsnAs 355

Db       1032 TGGATATTGCATAGCTGATGGACAGAGGATGTTGGTTTATGAGTTTGTTCCTAACAAAAC 1091

Qy        355 nLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLeuLy 375
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Db       1092 TTTGGAATATCATCTTCATGGGAAAAATCTTCCGGTAATGGAGTTCTCCACTAGGTTGCG 1151

Qy        375 sIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsnProLysIl 395

Db       1152 TATCGCCTTAGGTGCTGCGAAAGGACTCGCTTACCTTCACGAAGACTGCCATCCTCGGAT 1211

Qy        395 eIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLysVa 415

Db       1212 CATTCACCGCGACATCAAGTCTGCAAATATTCTCTTGGACTTCAACTTTGATGCTATGGT 1271

Qy        415 lAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrArgVa 435

Db       1272 GGCTGATTTTGGATTAGCTAAGTTAACATCTGATAACAACACTCATGTATCTACTCGTGT 1331

Qy        435 lMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGluLy 455

Db       1332 GATGGGAACTTTCGGATATCTAGCTCCAGAATATGCTTCAAGCGGTAAATTAACCGAGAA 1391

Qy        455 sSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgProVa 475

Db       1392 ATCCGATGTTTTCTCTTACGGAGTTATGTTATTGGAACTTATAACTGGAAAACGACCGGT 1451

Qy        475 lAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgProLeuLeuAs 495

Db       1452 TGAT---AATAGCATCACCATGGACGACACCTTAGTAGATTGGGCTCGGCCTCTTATGGC 1508

Qy        495 nArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsnAsnGlyTy 515

Db       1509 TCGCGCGCTAGAAGATGGAAACTTTAATGAGCTCGCAGATGCGAGGCTTGAAGGCAACTA 1568

Qy        515 rAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArgHisSerAl 535

Db       1569 CAACCCGCAAGAAATGGCTCGAATGGTGACTTGTGCCGCTGCTAGCATTCGTCATTCGGG 1628

Qy        535 aArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnValSerLeuSe 555

Db       1629 GCGTAAACGTCCAAAGATGAGCCAGATAGTAAGAGCGTTAGAAGGAGAAGTGTCCTTAGA 1688

Qy        555 rAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyrGlyGlySe 575

Db       1689 TGCTTTAAACGAAGGTGTGAAGCCAGGACACAGTAACGTTTACGGGTCATTGGGAGCAAG 1748

Qy        575 rThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLysMetAlaLe 595

Db       1749 CTCGGATTATAGTCAGACATCTTACAATGCAGACATGAAGAAATTCAGACAGATAGCTTT 1808

Qy        595 uGlyThrGlnGluTyr---------AsnAlaThrGlyGluTyrSerAsnProThrSerAs 612

Db       1809 GTCGAGCCAAGAATTCCCAGTCAGTGACTGTGAAGGAACATCTAGTAATGATTCTAGAGA 1868

Qy        612 pTyrGly 614

Db       1869 TATGGGA 1875

RESULT 8
US-10-086-464-9
; Sequence 9, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
;  APPLICANT: GORING, Daphne R. et al.
;  TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
;  FILE REFERENCE: P 25,762-A USA
;  CURRENT APPLICATION NUMBER: US/10/086,464
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 10/069,304
;  PRIOR FILING DATE: 2002-02-19
;  PRIOR APPLICATION NUMBER: PCT/CA00/00966
;  PRIOR FILING DATE: 2000-08-18
;  PRIOR APPLICATION NUMBER: US 60/149,466
;  PRIOR FILING DATE: 1999-08-19
;  PRIOR APPLICATION NUMBER: US 60/159,122
;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 1939
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-10-086-464-9

Alignment Scores:
Pred. No.:                5.99e-105      Length:          1939
Score:                    1748.50        Matches:         367
Percent Similarity:       69.67%         Conservative:    81
Best Local Similarity:    57.08%         Mismatches:      141
Query Match:              50.64%         Indels:          55
DB:                       14             Gaps:            16

US-10-086-464-2 (1-647) x US-10-086-464-9 (1-1939)

Qy          3 SerAlaProSerProGlyThrGlySerProProSerProProSerAsnSerThrThrThr 22

Db         36 TCTGCTCCTCCAACAAACTCCACCTCTTCTCCATCTCCACCGTCTAATACCAATTCAACC 95

Qy         23 ThrProProProAlaSerAlaProProProThrThrProSerSerProProProProSer 42

Db         96 ACCTCTTCTCCG---------CCGGCTCCGTCTCCTCCTTCTCCTACACCTCCTCAAGGA 146

Qy         43 ThrIleProThrSerProProProSerSerArgSerThrProSerAlaProProProSer 62

Db        147 GACTCATCATCATCGCCACCTCCTGATTCCACATCTCCACCAGCTCCACAAGCTCCTAAC 206

Qy         63 ProProThrProSerThrProGlySerProProProLeuProGlnProSerProProAla 82

Db        207 CCTCCTAAT---TCCTCTAATAACTCTCCTTCCCCTCCGTCACAGGGCGGTGGAGGAGAA 263

Qy         83 ProThrThrProGlySerProProAlaProValThrProProThrArgAsnProProPro 102

Db        264 AGAGGAAATGGAGGAAACAATGGTGGCAATGATACTCCACCGTCACGCGGCTCTCCTCCT 323

Qy        103 SerValProGlyProProSerAsnProSerArgGluGlyGlySerProArg------Pro 120

Db        324 TCT---------CCTCCTTCTAGGAGTAATGGAGATAATGGTGGTAGCAGATCATCGCCA 374

Qy        121 ProSer-----------------SerProSerProProSerPro------SerSerAsp 132

Db        375 CCAGGAGACACTGGAGGCTCTCGCTCAGACAACCCTCCTTCTAGCGGAGGAAGCAGTGGA 434

Qy        133 Gly--------------------LeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        435 GGAGGTGGAGGTGGAAGAAGTAATACGAATACAGCGATCATAGTTGGTGTATTAGTCGGA 494

Qy        146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165

Db        495 GCTGGACTTTTGATGATCGTTCTTATTATTGTGTGTCTTAGACGCAAAAAGAAGAGAAAA 554

Qy        166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyProLysAlaGly 185

Db        555 -----------GACTCCTTCTAC-----------------CCTGAACCCATGAAAGGA 584

Qy        186 GlyProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGlnAsnAlaThrProProSerAsp 205

Db        585 AACCAATAT---------CAATACTA-TGGAAACAACAACAACAACAATGCTTCACAGAA 634

Qy        206 HisValValThrSerLeuProProProProLysAlaProSerProPro------------ 221

Db        635 ------TTATCCGAATTGGCACCTAAATTCACAAGGCCAAAACCAACAATCTACTGGTGG 688

Qy        222 ------ArgGln-ProProProProProProProProPheMetSerSerSerGly----- 237

Db        689 TTGGGGAGGCGGTGGACCATCACCGCCTCCTCCTCCGCGGATGCCTACAAGCGGAGAAGA 748

Qy        238 -GlySerAspTyrSer------AspArgProValLeuProProProSerProGlyLeuVa 255

Db        749 TTCTTCCATGTACTCAGGCCCATCACGCCCAGTTTTACCTCCTCCTTCGCCTGCTCTAGC 808
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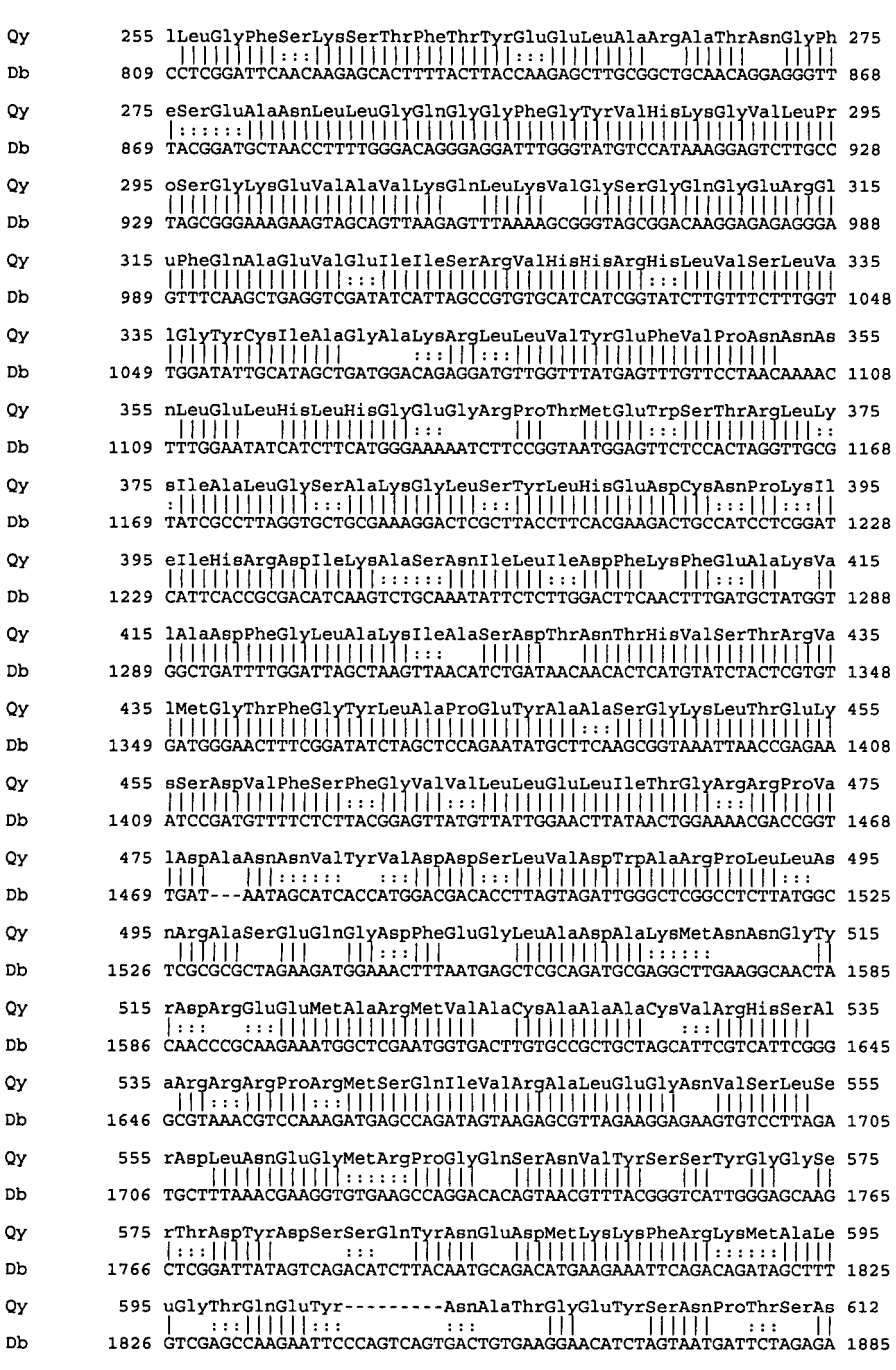

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Qy        612 pTyrGly 614
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Db       1886 TATGGGA 1892
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RESULT 9
US-10-425-114-9117
; Sequence 9117, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9117
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700833950_FLI
US-10-425-114-9117

Alignment Scores:

Pred. No.:	2.31e-104	Length:	1424
Score:	1737.50	Matches:	331
Percent Similarity:	88.73%	Conservative:	47
Best Local Similarity:	77.70%	Mismatches:	41
Query Match:	50.32%	Indels:	7
DB:	13	Gaps:	4

US-10-086-464-2 (1-647) x US-10-425-114-9117 (1-1424)

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Qy        226 ProProProProProProPheMetSerSerSerGly------GlySerAspTyrSerAsp 243
                                                  ||||||::: |||
Db         12 CCCCCACCACCGCCTCCTTTCATCAGCAGCAGTGGCGGATCTGGATCAAACAATTCAGGC 71

Qy        244 ArgProValLeuProProProSerProGlyLeuValLeuGlyPheSerLysSerThrPhe 263
                                                  |||||||||||||||||||||||||
Db         72 GGTGAATTTCTTCCTCCTCCTTCTCCAGGAATTTCATTGGGGTTCTCTAAGAGCACATTC 131

Qy        264 ThrTyrGluGluLeuAlaArgAlaThrAsnGlyPheSerGluAlaAsnLeuLeuGlyGln 283
                                                  |||||||||||||||||||||||||
Db        132 ACGTATGAGGAGTTGGCACGCGCAACTGATGGCTTCTCTGATGCCAACCTCCTTGGACAA 191

Qy        284 GlyGlyPheGlyTyrValHisLysGlyValLeuProSerGlyLysGluValAlaValLys 303
                                                  |||||||||||||||||||||||||
Db        192 GGAGGATTTGGATATGTGCACAGAGGAATTCTTCCCAACGGCAAGGAGGTGGCAGTGAAG 251

Qy        304 GlnLeuLysValGlySerGlyGlnGlyGluArgGluPheGlnAlaGluValGluIleIle 323
                                                  |||||||||||||||||||||||||
Db        252 CAATTGAAGGCTGGAAGCGGGCAAGGGGAGCGTGAATTCCAAGCTGAAGTTGAGATAATT 311

Qy        324 SerArgValHisHisArgHisLeuValSerLeuValGlyTyrCysIleAlaGlyAlaLys 343
                                                  |||||||||||||||||||||||||
Db        312 AGCCGTGTCCATCACAAGCATCTTGTTTCTTTGGTTGGATACTGCATCACTGGGTCCCAG 371

Qy        344 ArgLeuLeuValTyrGluPheValProAsnAsnAsnLeuGluLeuHisLeuHisGlyGlu 363
                                                  |||||||||||||||||||||||||
Db        372 AGGCTGCTTGTTTATGAATTTGTTCCCAACAACACATTGGAATTCCATTTGCATGGAAAA 431

Qy        364 GlyArgProThrMetGluTrpSerThrArgLeuLysIleAlaLeuGlySerAlaLysGly 383
                                                  |||||||||||||||||||||||||
Db        432 GGGAGACCTACCATGGATTGGCCCACAAGACTAAGAATTGCTTTAGGATCTGCTAAGGGA 491

Qy        384 LeuSerTyrLeuHisGluAspCysAsnProLysIleIleHisArgAspIleLysAlaSer 403
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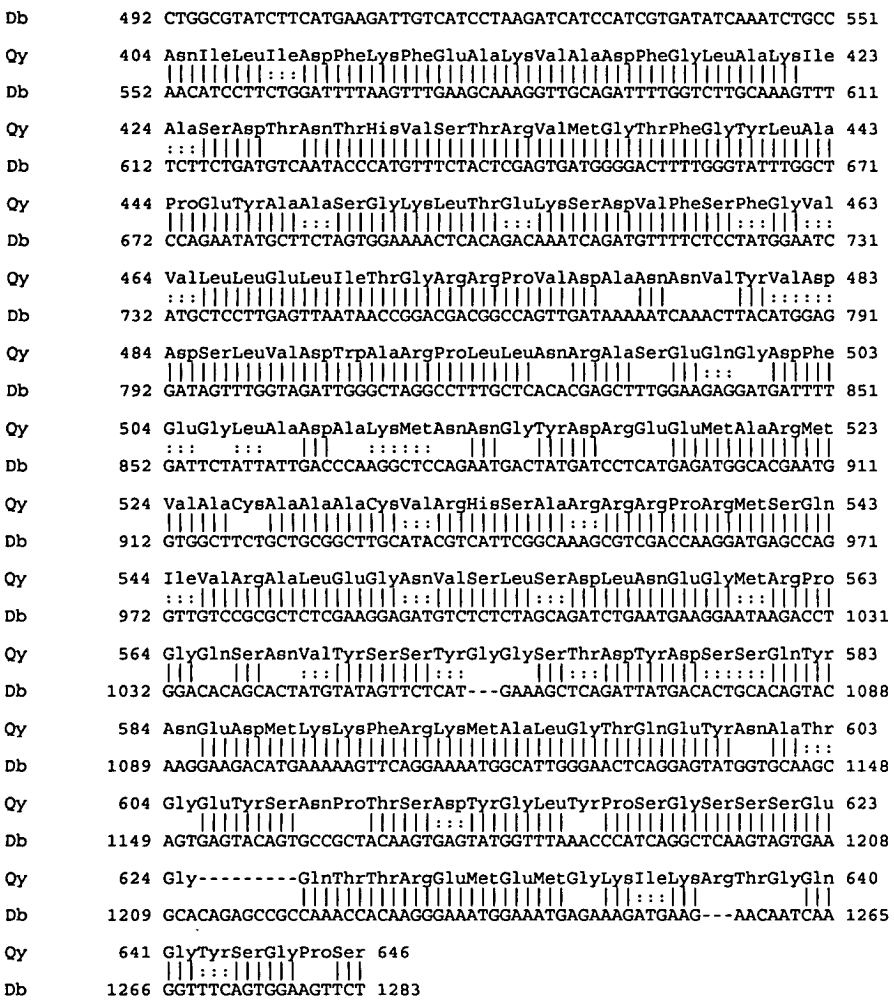
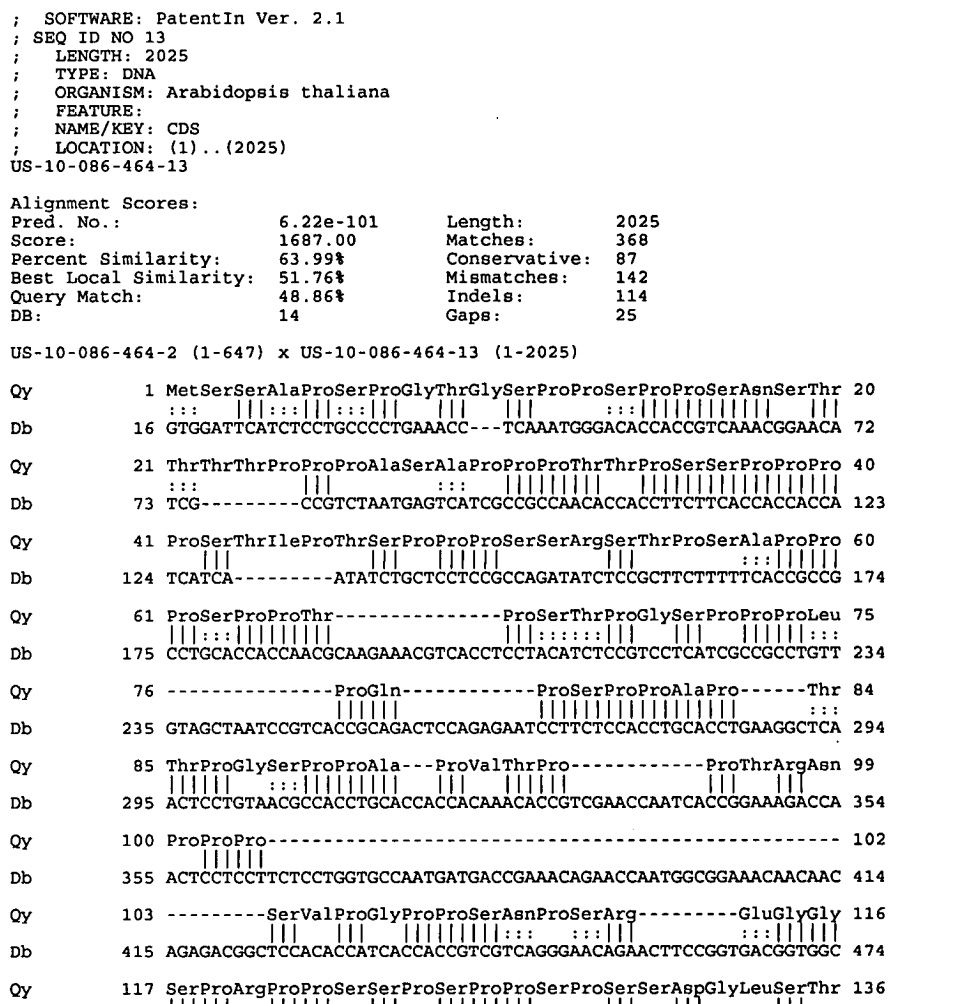


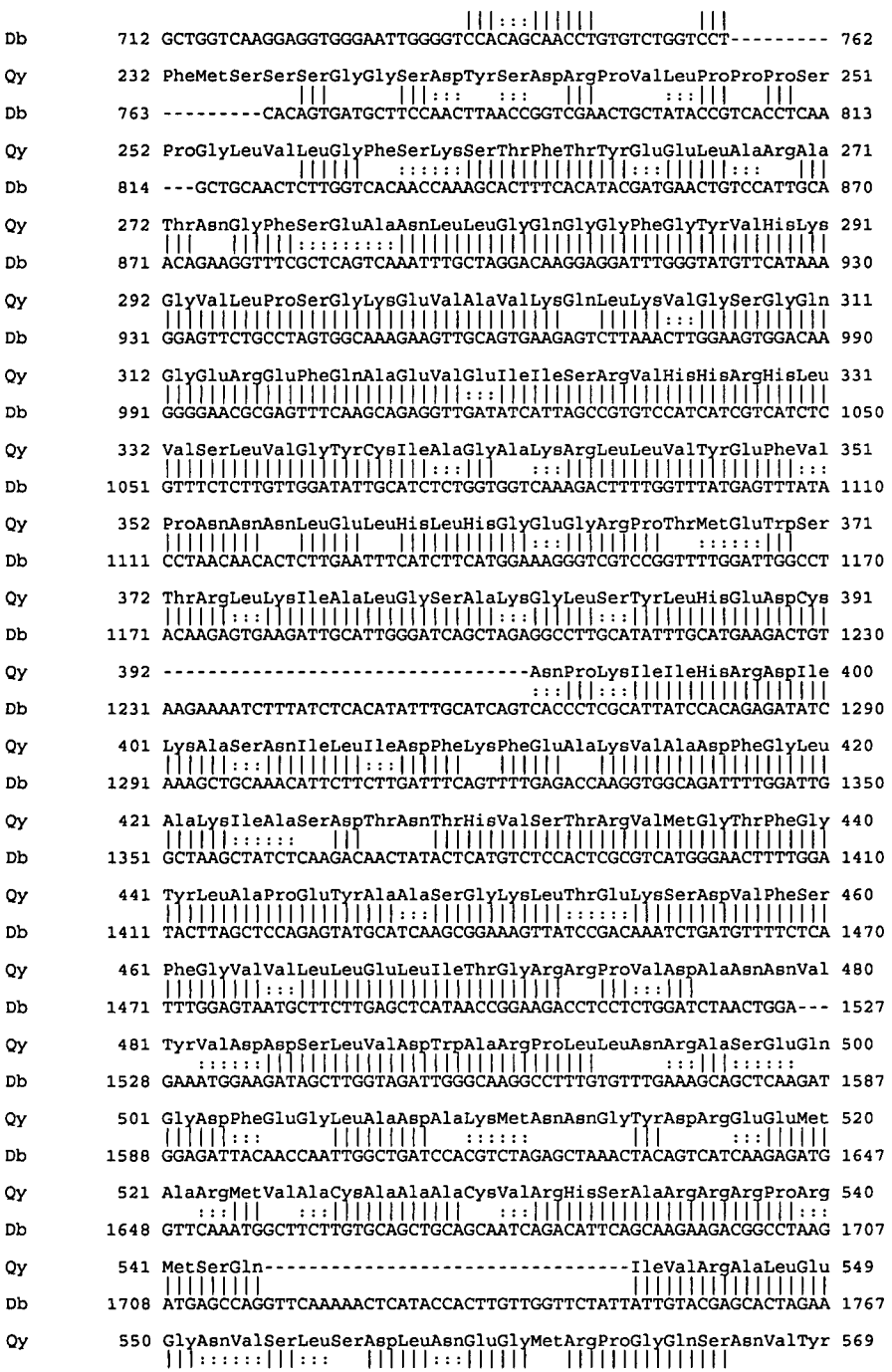
RESULT 10
US-10-086-464-13
; Sequence 13, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2025)
US-10-086-464-13

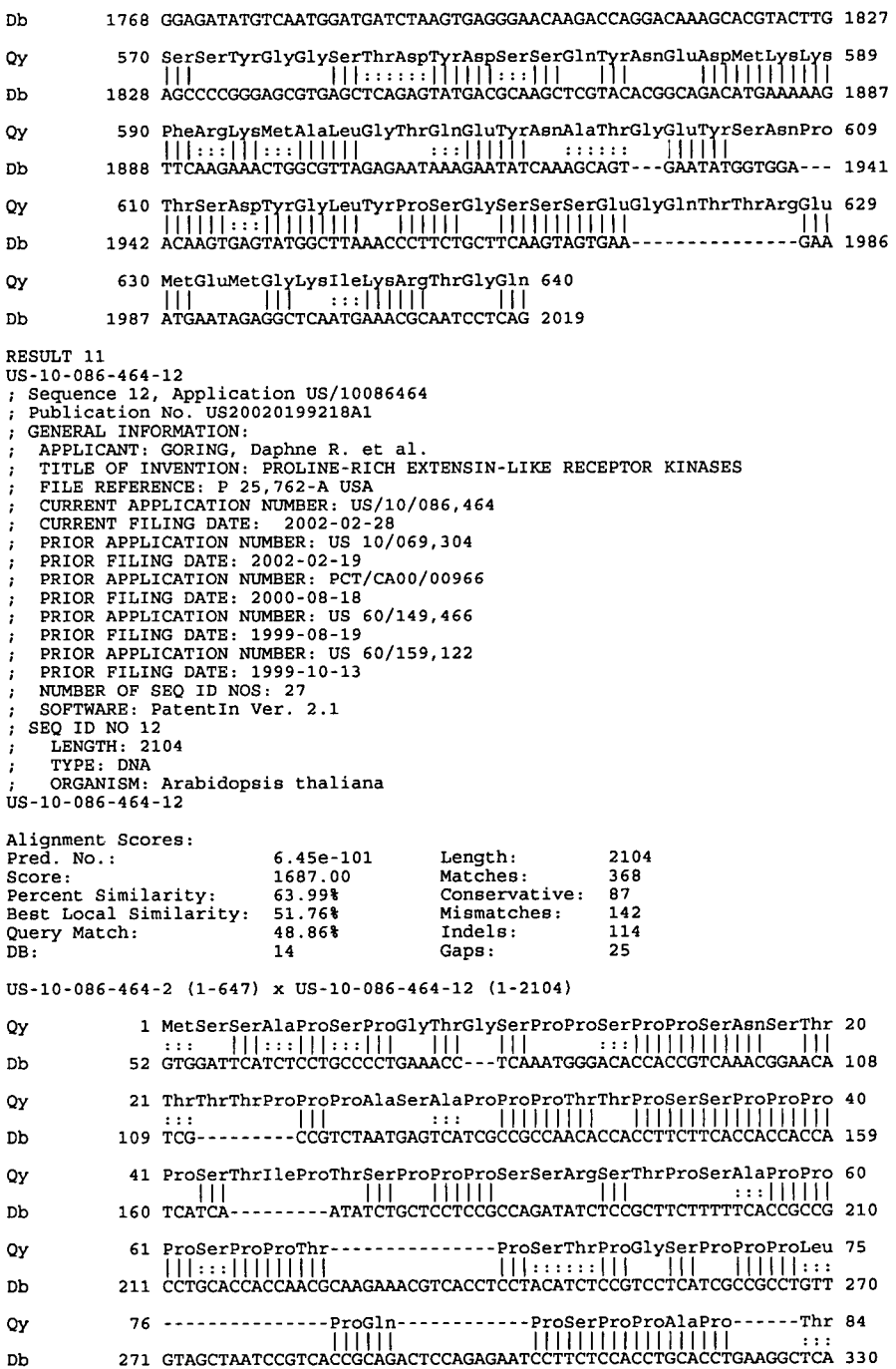
Alignment Scores:

Pred. No.:	6.22e-101	Length:	2025
Score:	1687.00	Matches:	368
Percent Similarity:	63.99%	Conservative:	87
Best Local Similarity:	51.76%	Mismatches:	142
Query Match:	48.86%	Indels:	114
DB:	14	Gaps:	25

US-10-086-464-2 (1-647) x US-10-086-464-13 (1-2025)





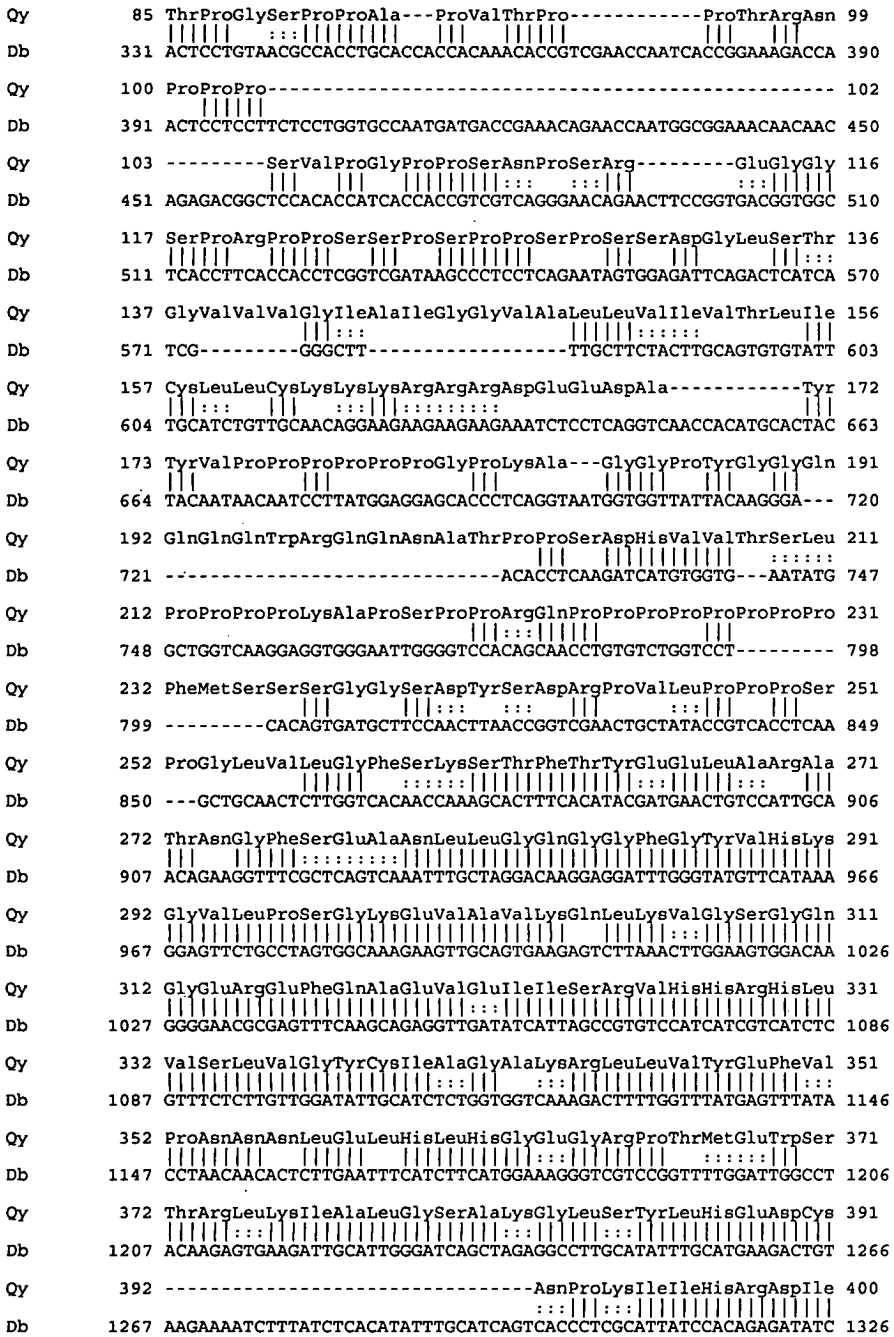


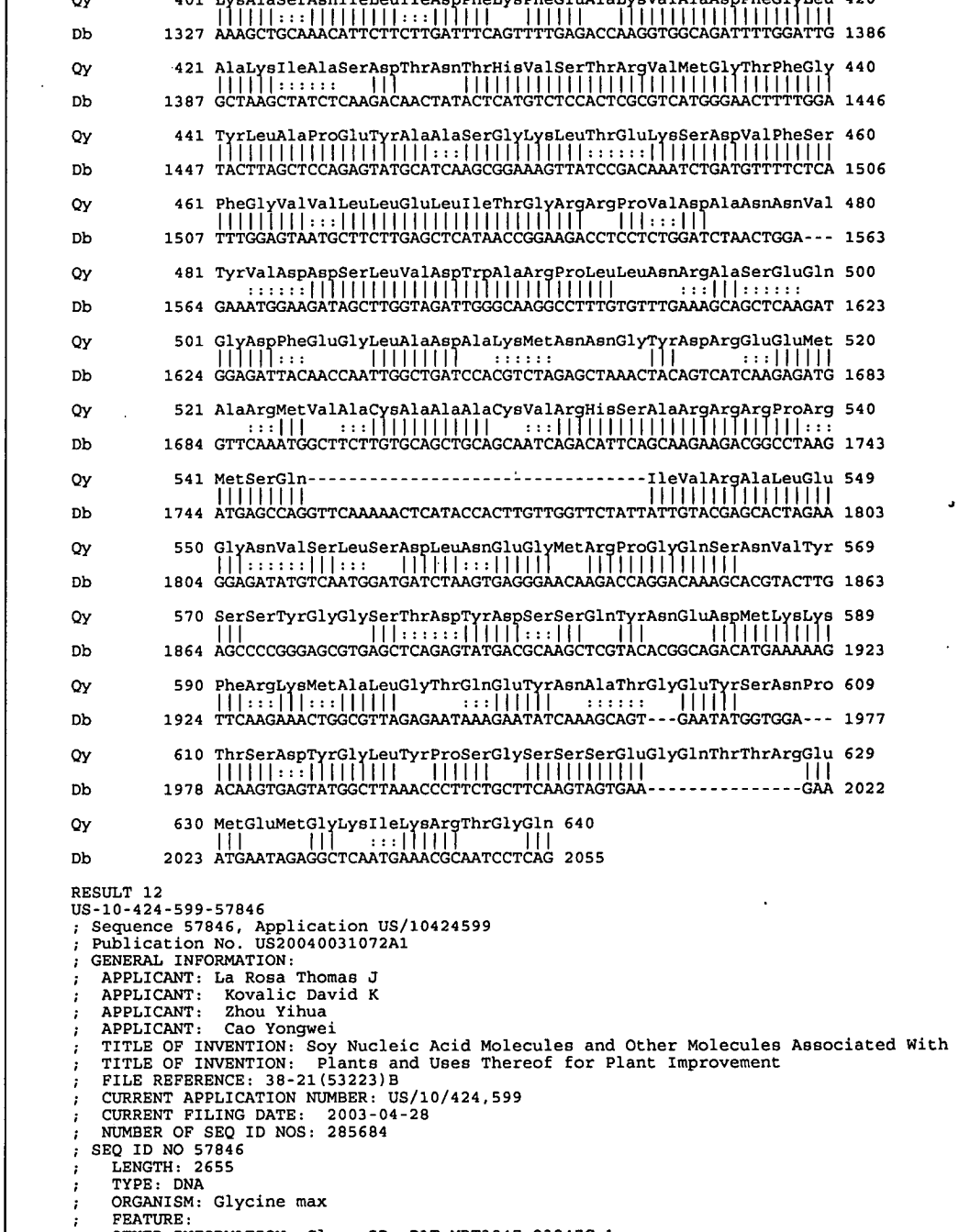
RESULT 11
US-10-086-464-12
; Sequence 12, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-086-464-12

Alignment Scores:

Pred. No.:	6.45e-101	Length:	2104
Score:	1687.00	Matches:	368
Percent Similarity:	63.99%	Conservative:	87
Best Local Similarity:	51.76%	Mismatches:	142
Query Match:	48.86%	Indels:	114
DB:	14	Gaps:	25

US-10-086-464-2 (1-647) x US-10-086-464-12 (1-2104)





RESULT 12
US-10-424-599-57846
; Sequence 57846, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57846
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23247C.1

US-10-424-599-57846

Alignment Scores:

Pred. No.:	3.37e-91	Length:	2655
Score:	1539.00	Matches:	341
Percent Similarity:	55.19%	Conservative:	95
Best Local Similarity:	43.16%	Mismatches:	141
Query Match:	44.57%	Indels:	213
DB:	13	Gaps:	19

US-10-086-464-2 (1-647) x US-10-424-599-57846 (1-2655)

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Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSer------ 19
              ||||||:::|||:::     |||  :::||||||||||||||||||:::|||
Db         98 TCATCTTCTCCAACA---AACACTTCCACCCCACCATCACCTCCCAGTTCTTCTCAGCCT 154

Qy         20 -----------ThrThrThrThrProProProAlaSerAlaPro---ProProThrThr 34
                        |||  |||      |||  :::  ||||||     |||:::
Db        155 AATCAAACACAAACACAAACACAAACACCCAATTCCCCTGCTCCTTCATCTCCTTCTGAC 214

Qy         35 ProSerSerProPro------ProProSerThrIleProThrSerProProProSerSer 52
              ||||||:::||||||      ||||||      :::|||   :::||||||||||||
Db        215 CCTTCTGCTCCACCTCCTTCTCCTCCTCAGGCAGTGCCATTAACCCCTCCTCCTTCCATA 274

Qy         53 ArgSerThrPro---------SerAlaProProProSerProProThrProSerThrPro 69
                 :::|||         |||   |||||||||:::   |||  ||||||   |||
Db        275 TCACTGTCTCCTCCACCATCATCTACACCACCACCAACTTTGCCCCCTCCATCACCACCT 334

Qy         70 GlySerProProProLeuPro--------------------------------GlnPro 78
              ||||||||||||||||||                                    |||
Db        335 GATTCTCCACCACCATTGCCACCTGCATCTCCAACCCCACCAGTTACAACATCTCCCCCC 394

Qy         79 SerProProAlaProThrThrProGlySerProProAlaProValThrProProThrArg 98
              |||||||||      |||:::|||   ||||||||||||      :::||||||
Db        395 TCACCACCAGTTACAACATCTCCCCCCTCACCACCAGCTACCACATCCCCTCCTCCAGCT 454

Qy         99 AsnProProProSerValPro------GlyProProSerAsnProSerArgGluGlyGly 116
                    |||||||||:::|||         |||||||||   |||:::          |||
Db        455 GAAACTCCACCTTCCCTTCCAAATTTGTCTCCACCATCTCCACCAGCC---------GGT 505

Qy        117 SerProArgPro-------------------------------------ProSerSerPro 124
              ||||||   |||                                     |||   ||||||
Db        506 TCCCCTCCTCCTCAATCACCTCCCACAACAATTCCACCTCCCTCTCGACCGATTTCGCCA 565

Qy        125 SerProProSerProSer---------------------------------------- 130
              |||||||||   |||:::
Db        566 TCTCCTCCTCCTCCGGCCAATTTTCCAAGGCCACCAACCACTAGAACTCCTCCAGAGAAA 625

Qy        130 ---------------------------------------------------------- 130

Db        626 GAAAATCCACCAAAAACTACTCCTTCACATGCATCTCCTCCATCAGTTTCTGAAACTCCT 685

Qy        130 ---------------------------------------------------------- 130

Db        686 CCTAAACCTCCTTCCTCTGATGTTCCCCCTCCATCCACATTGCCTTCAACTCCTCCTTCA 745

Qy        130 ---------------------------------------------------------- 130

Db        746 GACCCTTCAGGATCTTCACCTCCAGCTTCTTTGCCTGATCCCCCAACTAATAAAACAGTG 805

Qy        130 ---------------------------------------------------------- 130

Db        806 GTGGGGGGTCCGAAGGTGTCGCTACCCTCTCTTCCAACTGAGAAACCCACTGCTAGACCT 865

Qy        131 -------------------------------------------------SerAspGlyLeu 134
                                                              |||  ||||||
Db        866 ACTAATGATGGTACTAACAGTATGTCTTCAAACAACACACCTTCACATTCTGGAGGGTTG 925

Qy        135 SerThrGly------ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIle 152
              |||||||||      |||   :::||||||   :::|||   :::   |||   ::::::
Db        926 AGCACTGGAGGATCTGTGGCTATTGGAATTGTAGTTGGTTTTATTGTCCTCAGCCTTCTT 985

Qy        153 ValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAlaTyr 172
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                 |||      :::            |||||||||::::::
Db         986 GTTATGGCTGTGTGGTTTGCACAGAAGAAAAAGAAGAAGGGAACAGGATCAAGAGGTAGT 1045

Qy         173 TyrValProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGln 192
                 |||      |||   |||
Db        1046 TATGCTGCTCCTTCTCCA---------------------------------------- 1063

Qy         193 GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212
                                                  |||   |||         :::|||
Db        1064 --------------------------TTACCTCATCCCACAATTCAGGTACCTTATTC 1096

Qy         213 ProProProLysAlaProSerProProArgGlnProProProProProProProProPhe 232
                    |||::::::|||:::                                     |||
Db        1097 TTGAGGCCGCAGTCTCCGGCC---------------------------------AACTTT 1123

Qy         233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro 252
                :::   |||       |||||||||:::          |||       |||       |||
Db        1124 TTAGGTAGTGGCTCTGGTAGTGATTTT-----------GTATATTCTCCATCAGAGCCT 1171

Qy         253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272
                |||   |||         |||:::|||   |||||||||||||||||   :::|||||||
Db        1172 GGTGGTGTA---AGTAGTTCAAGATCATGGTTCACATATGAAGAACTTATTCAAGCTACA 1228

Qy         273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
                |||||||||||      |||||||||||:::|||||||||||   |||:::||||||
Db        1229 AATGGGTTTTCAGCACAAAATTTGTTGGGAGAAGGTGGATTTGGCTGTGTTTATAAAGGT 1288

Qy         293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312
                :::|||      |||:::|||||||||||||||||||||:::|||   |||||||||
Db        1289 TTGCTGATAGATGGAAGAGAAGTAGCTGTGAAACAGCTCAAAATTGGTGGTGGGCAAGGG 1348

Qy         313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332
                |||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db        1349 GAACGCGAATTCAGGGCAGAAGTTGAGATTATTAGCCGTGTACATCATCGTCATCTGGTT 1408

Qy         333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352
                |||||||||||||||||||||:::      :::|||||||||||||||:::::|||||||
Db        1409 TCTTTAGTTGGTTACTGTATATCCGAGCATCAGAGATTGCTTGTATATGACTATGTTCCC 1468

Qy         353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372
                |||:::   |||      ||||||||||||||   ||||||   :::::|||   |||
Db        1469 AACGATACTCTTCATTACCATCTCCACGGTGAAAATAGACCAGTTCTAGATTGGCCTACC 1528

Qy         373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392
                |||:::|||:::|||   |||:::|||:::|||:::::|||||||||||||||||:::
Db        1529 AGAGTCAAGGTTGCTGCTGGTGCAGCTCGTGGAATAGCTTACTTGCATGAAGACTGTCAT 1588

Qy         393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412
                |||:::|||||||||||||||||||:::|||||||||||:::|||      :::|||
Db        1589 CCACGCATTATTCATCGAGATATTAAGTCATCAAACATCCTACTTGATCTCAACTATGAA 1648

Qy         413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432
                |||:::|||:::|||||||||||||||||:::|||   |||:::|||||||||||:::
Db        1649 GCTCAAGTTTCGGACTTTGGGCTTGCAAAATTGGCATTAGATTCAAATACACATGTAACT 1708

Qy         433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452
                |||||||||||||||||||||||||:::|||||||||||||||   |||||||||||
Db        1709 ACACGTGTAATGGGAACCTTTGGGTACATGGCACCAGAATATGCGACAAGTGGAAAACTT 1768

Qy         453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472
                |||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        1769 ACTGAAAAGTCTGATGTATATTCTTTTGGGGTTGTGCTTTTGGAGCTAATTACAGGTCGG 1828

Qy         473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492
                :::||||||||||||:::          |||:::|||||||||:::||||||||||||
Db        1829 AAGCCTGTAGATGCATCTCAACCAATTGGTGATGAGAGCCTGGTTGAATGGGCTCGACCT 1888

Qy         493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512
                ||||||      |||   :::      |||||||||   |||   |||   ::::::
Db        1889 CTGTTGACGGAAGCACTTGACAATGAGGACTTTGAAATTTTGGTGGATCCAAGACTGGGG 1948

Qy         513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532
                   |||||||||   ||||||   |||||||:::      ||||||||||||||||||
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Db       1949 AAGAACTACGATAGAAATGAAATGTTTCGGATGATCGAGGCTGCCGCAGCCTGTGTACGC 2008

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552

Db       2009 CACTCATCGGTGAAGAGACCACGCATGAGTCAGGTGGTGAGAGCTTTAGATTCCTTGGAT 2068

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572

Db       2069 GAGTTTACGGATCTCAATAACGGAATGAAACCGGGACAGAGTTCGGTG------------ 2116

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592

Db       2117 --------------TTTGATTCGGCGCAGCAATCTGCACAAATCAGAATGTTTAGGAGG 2161

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612

Db       2162 ATGGCTTTTGGGAGCCAAGAT------AGTTCCGGTTTCTTCAATGAGTCTCAGAGTAGC 2215

Qy        613 Tyr-GlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMe 632

Db       2216 TGGAGGAGTA----------------------GAGATCACGACCCAACAACTGTCTTC 2251

Qy        632 tGlyLysIleLysArgThrGlyGlnGly 641

Db       2252 TCCCAAAATAAAA---CTGGGCATGGGA 2276

RESULT 13
US-10-425-114-7339
; Sequence 7339, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7339
;   LENGTH: 2655
;   TYPE: DNA
;  ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700652889_FLI
US-10-425-114-7339

Alignment Scores:
Pred. No.:              3.37e-91        Length:         2655
Score:                  1539.00         Matches:        341
Percent Similarity:     55.19%          Conservative:   95
Best Local Similarity:  43.16%          Mismatches:     141
Query Match:            44.57%          Indels:         213
DB:                     13              Gaps:           19

US-10-086-464-2 (1-647) x US-10-425-114-7339 (1-2655)

Qy          2 SerSerAlaProSerProGlyThrGlySerProProSerProProSerAsnSer------ 19

Db         98 TCATCTTCTCCAACA---AACACTTCCACCCCACCATCACCTCCCAGTTCTTCTCAGCCT 154

Qy         20 ------------ThrThrThrThrProProProAlaSerAlaPro---ProProThrThr 34

Db        155 AATCAAACACAAACACAAACACAAACACCCAATTCCCCTGCTCCTTCATCTCCTTCTGAC 214

Qy         35 ProSerSerProPro------ProProSerThrIleProThrSerProProProSerSer 52

Db        215 CCTTCTGCTCCACCTCCTTCTCCTCCTCAGGCAGTGCCATTAACCCCTCCTCCTTCCATA 274

Qy         53 ArgSerThrPro---------SerAlaProProProSerProProThrProSerThrPro 69

Db        275 TCACTGTCTCCTCCACCATCATCTACACCACCACCAACTTTGCCCCCTCCATCACCACCT 334

Qy         70 GlySerProProProLeuPro--------------------------------GlnPro 78

Db        335 GATTCTCCACCACCATTGCCACCTGCATCTCCAACCCCACCAGTTACAACATCTCCCCCC 394

Qy         79 SerProProAlaProThrThrProGlySerProProAlaProValThrProProThrArg 98

Db        395 TCACCACCAGTTACAACATCTCCCCCTCACCACCAGCTACCACATCCCCTCCTCCAGCT 454

Qy         99 AsnProProProSerValPro------GlyProProSerAsnProSerArgGluGlyGly 116

Db        455 GAAACTCCACCTTCCCTTCCAAATTTGTCTCCACCATCTCCACCAGCC---------GGT 505

Qy        117 SerProArgPro------------------------------------ProSerSerPro 124

Db        506 TCCCCTCCTCCTCAATCACCTCCCACAACAATTCCACCTCCCTCTCGACCGATTTCGCCA 565

Qy        125 SerProProSerProSer---------------------------------------- 130

Db        566 TCTCCTCCTCCTCCGGCCAATTTTCCAAGGCCACCAACCACTAGAACTCCTCCAGAGAAA 625

Qy        130 ---------------------------------------------------------- 130

Db        626 GAAAATCCACCAAAAACTACTCCTTCACATGCATCTCCTCCATCAGTTTCTGAAACTCCT 685

Qy        130 ---------------------------------------------------------- 130

Db        686 CCTAAACCTCCTTCCTCTGATGTTCCCCCTCCATCCACATTGCCTTCAACTCCTCCTTCA 745

Qy        130 ---------------------------------------------------------- 130

Db        746 GACCCTTCAGGATCTTCACCTCCAGCTTCTTTGCCTGATCCCCCAACTAATAAAACAGTG 805

Qy        130 ---------------------------------------------------------- 130

Db        806 GTGGGGGGTCCGAAGGTGTCGCTACCCTCTCTTCCAACTGAGAAACCCACTGCTAGACCT 865

Qy        131 ----------------------------------------------SerAspGlyLeu 134

Db        866 ACTAATGATGGTACTAACAGTATGTCTTCAAACAACACACCTTCACATTCTGGAGGGTTG 925

Qy        135 SerThrGly------ValValValGlyIleAlaIleGlyGlyValAlaLeuLeuValIle 152

Db        926 AGCACTGGAGGATCTGTGGCTATTGGAATTGTAGTTGGTTTTATTGTCCTCAGCCTTCTT 985

Qy        153 ValThrLeuIleCysLeuLeuCysLysLysLysArgArgArgAspGluGluAspAlaTyr 172

Db        986 GTTATGGCTGTGTGGTTTGCACAGAAGAAAAAGAAGAAGGGAACAGGATCAAGAGGTAGT 1045

Qy        173 TyrValProProProProProProGlyProLysAlaGlyGlyProTyrGlyGlyGlnGln 192

Db       1046 TATGCTGCTCCTTCTCCA---------------------------------------- 1063

Qy        193 GlnGlnTrpArgGlnGlnAsnAlaThrProProSerAspHisValValThrSerLeuPro 212

Db       1064 --------------------------TTTACCTCATCCCACAATTCAGGTACCTTATTC 1096

Qy        213 ProProProLysAlaProSerProProArgGlnProProProProProProProPhe 232

Db       1097 TTGAGGCCGCAGTCTCCGGCC--------------------------------AACTTT 1123

Qy        233 MetSerSerSerGlyGlySerAspTyrSerAspArgProValLeuProProProSerPro 252

Db       1124 TTAGGTAGTGGCTCTGGTAGTGATTTT-----------GTATATTCTCCATCAGAGCCT 1171

Qy        253 GlyLeuValLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThr 272

Db       1172 GGTGGTGTA---AGTAGTTCAAGATCATGGTTCACATATGAAGAACTTATTCAAGCTACA 1228

Qy        273 AsnGlyPheSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGly 292
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Db       1229 AATGGGTTTTCAGCACAAAATTTGTTGGGAGAAGGTGGATTTGGCTGTGTTTATAAAGGT 1288

Qy        293 ValLeuProSerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGly 312

Db       1289 TTGCTGATAGATGGAAGAGAAGTAGCTGTGAAACAGCTCAAAATTGGTGGTGGGCAAGGG 1348

Qy        313 GluArgGluPheGlnAlaGluValGluIleIleSerArgValHisHisArgHisLeuVal 332

Db       1349 GAACGCGAATTCAGGGCAGAAGTTGAGATTATTAGCCGTGTACATCATCGTCATCTGGTT 1408

Qy        333 SerLeuValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValPro 352

Db       1409 TCTTTAGTTGGTTACTGTATATCCGAGCATCAGAGATTGCTTGTATATGACTATGTTCCC 1468

Qy        353 AsnAsnAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThr 372

Db       1469 AACGATACTCTTCATTACCATCTCCACGGTGAAAATAGACCAGTTCTAGATTGGCCTACC 1528

Qy        373 ArgLeuLysIleAlaLeuGlySerAlaLysGlyLeuSerTyrLeuHisGluAspCysAsn 392

Db       1529 AGAGTCAAGGTTGCTGCTGGTGCAGCTCGTGGAATAGCTTACTTGCATGAAGACTGTCAT 1588

Qy        393 ProLysIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGlu 412

Db       1589 CCACGCATTATTCATCGAGATATTAAGTCATCAAACATCCTACTTGATCTCAACTATGAA 1648

Qy        413 AlaLysValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSer 432

Db       1649 GCTCAAGTTTCGGACTTTGGGCTTGCAAAATTGGCATTAGATTCAAATACACATGTAACT 1708

Qy        433 ThrArgValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeu 452

Db       1709 ACACGTGTAATGGGAACCTTTGGGTACATGGCACCAGAATATGCGACAAGTGGAAAACTT 1768

Qy        453 ThrGluLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArg 472

Db       1769 ACTGAAAAGTCTGATGTATATTCTTTTGGGGTTGTGCTTTTGGAGCTAATTACAGGTCGG 1828

Qy        473 ArgProValAspAlaAsnAsnValTyrValAspAspSerLeuValAspTrpAlaArgPro 492

Db       1829 AAGCCTGTAGATGCATCTCAACCAATTGGTGATGAGAGCCTGGTTGAATGGGCTCGACCT 1888

Qy        493 LeuLeuAsnArgAlaSerGluGlnGlyAspPheGluGlyLeuAlaAspAlaLysMetAsn 512

Db       1889 CTGTTGACGGAAGCACTTGACAATGAGGACTTTGAAATTTTGGTGGATCCAAGACTGGGG 1948

Qy        513 AsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValArg 532

Db       1949 AAGAACTACGATAGAAATGAAATGTTTCGGATGATCGAGGCTGCCGCAGCCTGTGTACGC 2008

Qy        533 HisSerAlaArgArgArgProArgMetSerGlnIleValArgAlaLeuGluGlyAsnVal 552

Db       2009 CACTCATCGGTGAAGAGACCACGCATGAGTCAGGTGGTGAGAGCTTTAGATTCCTTGGAT 2068

Qy        553 SerLeuSerAspLeuAsnGluGlyMetArgProGlyGlnSerAsnValTyrSerSerTyr 572

Db       2069 GAGTTTACGGATCTCAATAACGGAATGAAACCGGGACAGAGTTCGGTG------------ 2116

Qy        573 GlyGlySerThrAspTyrAspSerSerGlnTyrAsnGluAspMetLysLysPheArgLys 592

Db       2117 --------------TTTGATTCGGCGCAGCAATCTGCACAAATCAGAATGTTTAGGAGG 2161

Qy        593 MetAlaLeuGlyThrGlnGluTyrAsnAlaThrGlyGluTyrSerAsnProThrSerAsp 612

Db       2162 ATGGCTTTTGGGAGCCAAGAT------AGTTCCGGTTTCTTCAATGAGTCTCAGAGTAGC 2215

Qy        613 Tyr-GlyLeuTyrProSerGlySerSerSerGluGlyGlnThrThrArgGluMetGluMe 632

Db       2216 TGGAGGAGTA----------------------GAGATCACGACCCAACAACTGTCTTC 2251

Qy        632 tGlyLysIleLysArgThrGlyGlnGly 641

Db       2252 TCCCAAAATAAAA---CTGGGCATGGGA 2276

RESULT 14
US-10-425-114-14127
; Sequence 14127, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14127
;   LENGTH: 2190
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB148-034-D5_FLI
US-10-425-114-14127

Alignment Scores:
Pred. No.:              1.11e-84        Length:         2190
Score:                  1437.50         Matches:        331
Percent Similarity:     61.90%          Conservative:   80
Best Local Similarity:  49.85%          Mismatches:     167
Query Match:            41.63%          Indels:         87
DB:                     13              Gaps:           19

US-10-086-464-2 (1-647) x US-10-425-114-14127 (1-2190)

Qy          1 MetSerSerAlaProSerProGlyThrGlySerProPro---------------------- 13

Db          2 ATGATGCCTTCTTCCCTCCCTCATTCTCGCTCGCCCCCATTCCACCTTCGACGACCCCTT 61

Qy         14 SerProProSerAsnSerThrThrThrThrProProProAlaSerAlaProPro------ 31

Db         62 TCTCCTTCTCCCTCCTCAATCACCTGCAGCGAAAAGGAAAAGGGTGTCAGACCGTAACTA 121

Qy         31 ------------------------------------------------------------ 31

Db        122 AGAGCTATTTAGCAATAATACATACATAGCTATACCCTCTTTAGGTCAAGAGGGTGGAGT 181

Qy         32 ---ProThrThrProSerSerProProProProSerThrIlePro--------------- 45

Db        182 TCTCCTTATTCGGAGGAAGAGCTCCATCCTCATTCTACAAGACCAAACCAATAAATGGCC 241

Qy         46 ThrSerProProProSerSerArgSerThrProSerAlaProProProSerProProThr 65

Db        242 TCTAGCCCACAGTCCTCGCCATCATCCTCCAAGAAGTCGCCGCCACCACAAGAAGCATCA 301

Qy         66 ProSerThrProGlySerProProProProLeuProGlnProSerProProAlaProThrThr 85

Db        302 GCTTTGGCGCCAAAATCATCTTCA------AAGTCACCCTCGCCACCAAAGGGTGAATCA 355

Qy         86 ProGlySerProProAlaProValThrProProThrArgAsnProProProSerValPro 105

Db        356 ---AATTCATCTCCCAGTCCCCCATCGAAATCGTCCCTGTCACCACCGCCACGACCAAAG 412

Qy        106 GlyProProSerAsnProSerArgGluGlyGlySerProArgProProSerSerProSer 125

Db        413 AAAAGTGCTAGTACATCTAGCTCTAAAGATGGGAAGACGAAGAAGTCGTCTTCATCGTCT 472

Qy        126 ProProSerProSerSerAspGlyLeuSerThrGlyValValValGlyIleAlaIleGly 145

Db        473 TCATCGTCGGATAATACAGCCGCTGTGATCACCGGCGTGGTGCTTGGGGTG---GTGGGC 529
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Qy       146 GlyValAlaLeuLeuValIleValThrLeuIleCysLeuLeuCysLysLysLysArgArg 165
Db       530 TTCGCTCTGCTCTTGTCCATCGTGGCGTGCGTGTGCTGCGCCAAGAAGAAGAAGAAACGT 589

Qy       166 ArgAspGluGluAspAlaTyrTyrValProProProProProProGlyPro--------- 182
Db       590 ----------------------------CCGCCCCCAATGAACATGCCCTTCTACACC 619

Qy       183 ---LysAlaGlyGly---------ProTyrGlyGlyGlnGlnGlnGlnTrpArgGlnGln 198
Db       620 GACGAGAAAGGCAATGTGTATTACCCCAACGCTGGTCTGCCGCCTATGTGGCAGCAATAT 679

Qy       199 AsnAlaThrProProSerAspHisValValThrSerLeuProProProProLysAlaPro 218
Db       680 GGCAGCAAC--------------------GGCAGCATCCCTCCGCCGGG-ATGGCACCA 717

Qy       219 SerProProArgGlnProPro-ProProProProProProPheMetSerSerSerGlyGl 238
Db       718 TCACGGCGGCGGGAACCCGCTGTCGCCATCGCTGGGCTCGATGGCGGCGCCCCTGAGCGG 777

Qy       238 ySerAspTyrSerAsp---------ArgProValLeuProProProSerProGlyLeuVa 255
Db       778 CGAGATGTACTCGTCCGGCCCCCACGGGCCTCCCCTCCCCCCACCTTCGCCGAACGTGGC 837

Qy       255 lLeuGlyPheSerLysSerThrPheThrTyrGluGluLeuAlaArgAlaThrAsnGlyPh 275
Db       838 GCTGGGGTTCTCCAAGAGCTCCTTCTCGTACGAGGAGCTAGCGGCAGCGACGTCGGGCTT 897

Qy       275 eSerGluAlaAsnLeuLeuGlyGlnGlyGlyPheGlyTyrValHisLysGlyValLeuPr 295
Db       898 CTCGTCGGCGAACCTGCTGGGGCAGGGCGGGTTCGGGTACGTGTACAAGGGCGTGCTCGC 957

Qy       295 o---SerGlyLysGluValAlaValLysGlnLeuLysValGlySerGlyGlnGlyGluAr 314
Db       958 CGGCAGCGGGAAGGAGGTGGCGGTGAAGCAGCTCAAGTCCGGGAGCGGGCAGGGGGAGCG 1017

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Qy       334 uValGlyTyrCysIleAlaGlyAlaLysArgLeuLeuValTyrGluPheValProAsnAs 354
Db       1078 CGTGGGCTACTGCATCGCGGGCAACCAGCGCATGCTCGTCTACGAGTTCGTGGCCAACAA 1137

Qy       354 nAsnLeuGluLeuHisLeuHisGlyGluGlyArgProThrMetGluTrpSerThrArgLe 374
Db       1138 CACGCTGGAGCACCATCTGTACGCCAAGGACGGCCCTGTCATGGACTGGAGCACCCGCAT 1197

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Db       1198 GAAGATCGCGCTCGGCTCCGCCAAGGGCCTCGCCTACCTCCACGAGGACTGCCATCCTCG 1257

Qy       394 sIleIleHisArgAspIleLysAlaSerAsnIleLeuIleAspPheLysPheGluAlaLy 414
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Qy       414 sValAlaAspPheGlyLeuAlaLysIleAlaSerAspThrAsnThrHisValSerThrAr 434
Db       1318 GGTGGCGGACTTCGGGCTGGCCAAGCTCACGACGGACACCAACACGCACGTCTCCACGCG 1377

Qy       434 gValMetGlyThrPheGlyTyrLeuAlaProGluTyrAlaAlaSerGlyLysLeuThrGl 454
Db       1378 CGTCATGGGCACCTTCGGCTACCTGGCGCCGGAGTACGCGTCCAGCGGCAAGCTCACGGA 1437

Qy       454 uLysSerAspValPheSerPheGlyValValLeuLeuGluLeuIleThrGlyArgArgPr 474
Db       1438 CAGGTCGGACGTCTTCTCCTTCGGCGTCATGCTGCTGGAGCTACTCACGGGGCGCCGCCC 1497

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Db       1498 CATCGATACCACCAAC---TACATGGAGGACAGCCTCGTGGACTGGGCGCGCCCGCTGCT 1554

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Db       1555 GAGCGCCGCGCTGGCGGGGGAGACGGGC---TTCGCCGAGCTCGTCGACCCCCGTCTGGG 1611

Qy       512 nAsnGlyTyrAspArgGluGluMetAlaArgMetValAlaCysAlaAlaAlaCysValAr 532
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Db       1672 CCACTCGGCCAAGCGCCGCCCCAAGATGAGCCAGATCGTGCGCGCGCTGGAGGGCGACGC 1731

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Db       1732 ATCGCTGGAGGATCTGCACCAGGACGGCGGCAAGCCCGGGCAGAGCGTGCTCTTCTCC-- 1789

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; Sequence 6300, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6300
;   LENGTH: 1500
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700560157_FLI
US-10-425-114-6300

Alignment Scores:
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Score:                  1437.00         Matches:        284
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US-10-086-464-2 (1-647) x US-10-425-114-6300 (1-1500)

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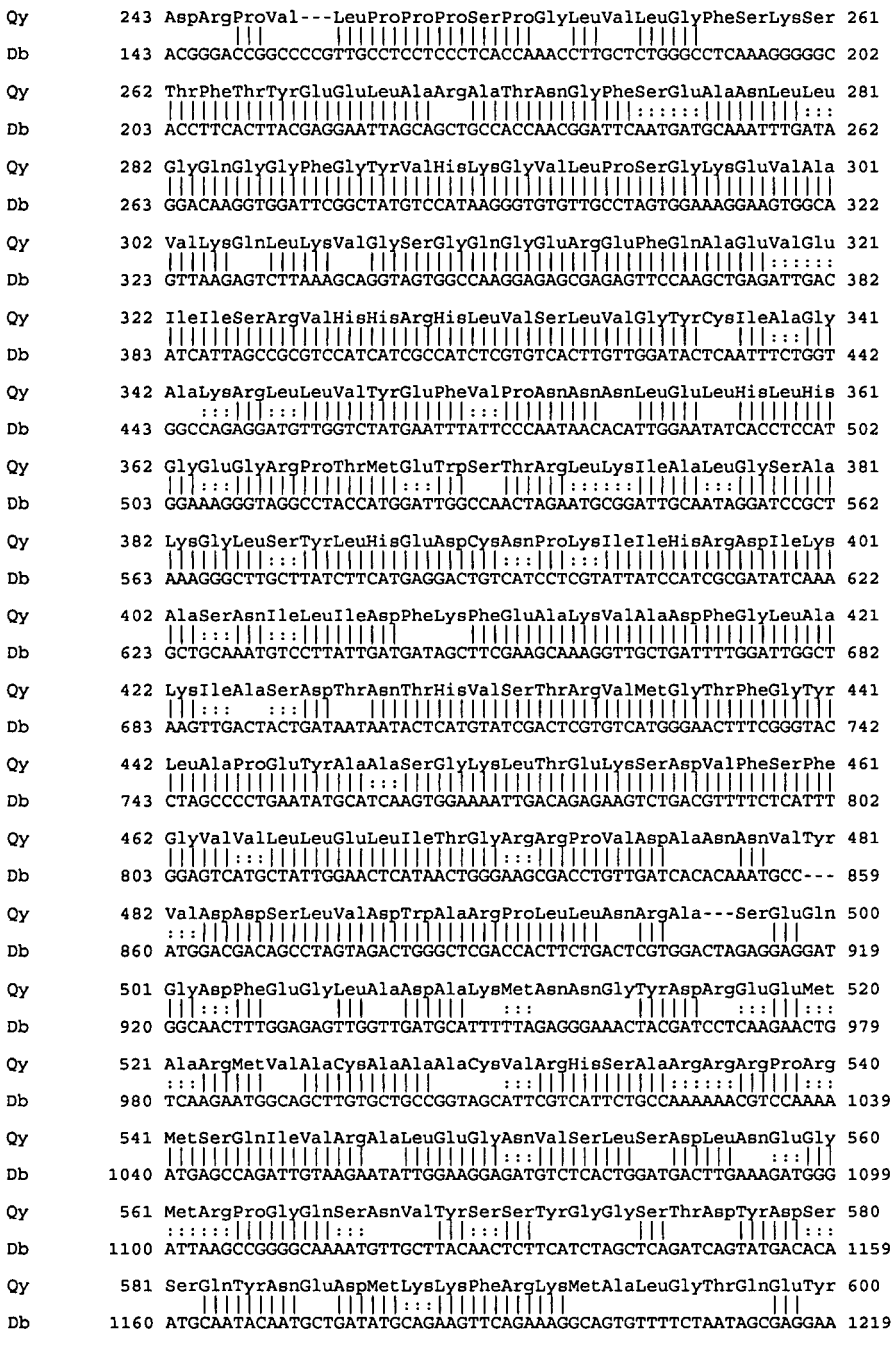

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2		1944	100.0	1944	6	AX825703	AX825703 Sequence
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17	c	26	1.3	47428	6	AX059540	AX059540 Sequence
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19		26	1.3	145453	8	AC012477	AC012477 Genomic S
20		26	1.3	183147	8	AC012392	AC012392 Genomic S
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ALIGNMENTS

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LOCUS AX088876 1944 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 1 from Patent WO0114563.
ACCESSION AX088876
VERSION AX088876.1 GI:13397639
KEYWORDS .
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1
AUTHORS Goring,D. and Silva,N.
TITLE Proline-rich extensin-like receptor kinases

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  JOURNAL   Patent: WO 0114563-A 1 01-MAR-2001;
            Goring, Daphne (CA) ; Silva, Nancy (CA)
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ORIGIN

  Query Match           100.0%;  Score 1944;  DB 6;  Length 1944;
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  Matches 1944;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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ACCESSION AX825703
VERSION AX825703.1 GI:39751230
KEYWORDS .
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1
AUTHORS Goring,D., Silva,N. and Haffani,Y.Z.
TITLE Increasing plant seed production
JOURNAL Patent: WO 03072763-A 1 04-SEP-2003;
Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1944; DB 6; Length 1944;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION   AX825705
VERSION     AX825705.1  GI:39751232
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 3 04-SEP-2003;
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Qy        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
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Qy        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
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Qy       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
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Qy       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
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RESULT 4
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DEFINITION  Brassica napus receptor protein kinase PERK1 mRNA, complete cds.
ACCESSION   AY028699
VERSION     AY028699.1  GI:13447448
KEYWORDS    .
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
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            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 2189)
  AUTHORS   Silva,N.F. and Goring,D.R.
  TITLE     Characterization of a novel Brassica napus receptor protein kinase
            PERK1
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2189)
  AUTHORS   Silva,N.F. and Goring,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-2001) Biology, York University, 4700 Keele
            Street, Toronto, Ontario M3J 1P3, Canada
FEATURES             Location/Qualifiers
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                     SPPRQPPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFS
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                     VGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCN
                     PKIIHRDIKASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFGYLAPEYAASG
                     KLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLAD
                     AKMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGMRPGQS
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ORIGIN

  Query Match           100.0%;  Score 1944;  DB 8;  Length 2189;
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  Matches 1944;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         97 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 156

Qy         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120
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Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180
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Qy        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240
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Qy        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300
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Qy        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360
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Qy        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420
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Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480
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Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576
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Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
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Qy        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660
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Qy        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720
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Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780
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Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900
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Qy        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960
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Qy        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
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Qy       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200
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Qy       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
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Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
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Qy       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500
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Qy       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
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Qy       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
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Qy       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
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Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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Db       2017 GGTTATAGTGGACCTTCTCTTTAA 2040
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RESULT 5
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DEFINITION  Sequence 36 from Patent WO03072763.
ACCESSION   AX825738
VERSION     AX825738.1  GI:39751255
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Goring,D., Silva,N. and Haffani,Y.Z.
  TITLE     Increasing plant seed production
  JOURNAL   Patent: WO 03072763-A 36 04-SEP-2003;
            Goring, Daphne (CA) ; Silva, Nancy (CA) ; Haffani, Yosr, Z. (CA)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             3.4%;  Score 66;  DB 6;  Length 1959;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       1492 TCTGAG 1497
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Db       1507 TCTGAG 1512


RESULT 6
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LOCUS       BT008400               1959 bp    mRNA    linear   PLN 15-MAY-2003
DEFINITION  Arabidopsis thaliana At3g24550 gene, complete cds.
ACCESSION   BT008400
VERSION     BT008400.1  GI:30725473
KEYWORDS    FLI_CDNA.
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SOURCE      Arabidopsis thaliana (thale cress)
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     The discrepancy does not affect the protein sequence.
            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
            Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J.,
            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     LCKKKRRRRHDDEAAYYVPPPPPSGPKAGGPYGGQQQYWQQQNASRPSDNHVVTSLPP
                     PKPPSPPRKPPPPPPPPAFMSSSGGSDYSDLPVLPPPSPGLVLGFSKSTFTYEELSRA
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                     HLVSLIGYCMAGVQRLLVYEFVPNNNLEFHLHGKGRPTMEWSTRLKIALGSAKGLSYL
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ORIGIN

  Query Match             3.4%;  Score 66;  DB 8;  Length 1959;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Db       1447 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1506

Qy       1492 TCTGAG 1497
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Db       1507 TCTGAG 1512


RESULT 7
BT008409
LOCUS       BT008409                1959 bp    mRNA    linear   PLN 15-MAY-2003
DEFINITION  Arabidopsis thaliana At3g24600 gene, complete cds.
ACCESSION   BT008409
VERSION     BT008409.1  GI:30725491
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Arabidopsis ORF clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1959)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
            Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
            Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L.,
            Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
            Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
            Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R.,
            Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M.,
            Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B.,
            Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J.,
            Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
            Yamada,K., Yu,G., Yuan,S., Davis,R.W.,  Theologis,A., and
            Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     YAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEEGDF
                     EGLADSKMGNEYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGM
                     RPGHSNVYSSYGGSTDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPSG
                     SSSEGQATREMEMGKIKKTGQGYSGPSL"
ORIGIN

  Query Match              3.4%;  Score 66;  DB 8;  Length 1959;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Db       1447 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1506

Qy       1492 TCTGAG 1497
             ||||||
Db       1507 TCTGAG 1512


RESULT 8
AY128792
LOCUS       AY128792               2098 bp    mRNA    linear   PLN 07-AUG-2002
DEFINITION  Arabidopsis thaliana protein kinase-like protein mRNA, complete
            cds.
ACCESSION   AY128792
VERSION     AY128792.1  GI:22136227
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            The RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the pUNI (ORF) clones using the RAFL cDNAs: Tripp,M.,
            Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R.,
            Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H.,
            Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Tripp,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
            to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="U16568"
                     /ecotype="Columbia"
                     /note="This clone is in pENTR/SD-dTopo  This is a cloned
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                     a template"
     CDS             1. .1959
                     /codon_start=1
                     /product="protein kinase-like protein"
                     /protein_id="AAM91192.1"
                     /db_xref="GI:22136228"
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                     EGLADSKMGNEYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGM
                     RPGHSNVYSSYGGSTDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPSG
                     SSSEGQATREMEMGKIKKTGQGYSGPSL"
ORIGIN

  Query Match              3.4%;  Score 66;  DB 8;  Length 2098;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Db       1447 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1506

Qy       1492 TCTGAG 1497
             ||||||
Db       1507 TCTGAG 1512


RESULT 9
AY056788
LOCUS       AY056788               2116 bp    mRNA    linear   PLN 08-OCT-2001
DEFINITION  Arabidopsis thaliana AT3g24550/MOB24_8 mRNA, complete cds.
ACCESSION   AY056788
VERSION     AY056788.1  GI:15983764
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2116)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
            Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
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  TITLE     Arabidopsis cDNA clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2116)
  AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
            Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
            Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
            Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,
            Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
            Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
            Davis,R.W., Theologis,A. and Ecker,J.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory
            (SIGnAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') :  Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P.,  Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H.,
            Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L.,
            Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G.,
            Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
            Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A.,
            Tang,C.C., Toriumi,M., Yamada,K., Yamamura, Y., Yu,G., Yu,S.,
            Davis,R.W.,  Theologis,A., and Ecker,J.R.

            Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
            this work.  Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     /db_xref="GI:15983765"
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                     LCKKKRRRRHDDEAAYYVPPPPPSGPKAGGPYGGQQQYWQQQNASRPSDNHVVTSLPP
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     3'UTR           1996. .2116
ORIGIN

  Query Match             3.4%;  Score 66;  DB 8;  Length 2116;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Qy       1492 TCTGAG 1497
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Db       1543 TCTGAG 1548


RESULT 10
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LOCUS       AY059901               2188 bp    mRNA    linear   PLN 04-NOV-2001
DEFINITION  Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
            complete cds.
ACCESSION   AY059901
VERSION     AY059901.1  GI:16649062
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2188)
  AUTHORS   Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2001) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Nguyen,M.,
            Southwick,A., Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     /chromosome="III"
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     gene            1. .2188
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     CDS             32. .1990
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ORIGIN

  Query Match             3.4%;  Score 66;  DB 8;  Length 2188;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Qy       1492 TCTGAG 1497
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Db       1538 TCTGAG 1543


RESULT 11
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LOCUS       AY093065                2190 bp    mRNA    linear   PLN 21-APR-2002
DEFINITION  Arabidopsis thaliana unknown protein (At3g24550) mRNA, complete
            cds.
ACCESSION   AY093065
VERSION     AY093065.1  GI:20260331
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2190)
  AUTHORS   Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Southwick,A.,
            Nguyen,M., Karlin-Neumann,G.,  Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford)  contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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                     SSSEGQATREMEMGKIKKTGQGYSGPSL"
ORIGIN

  Query Match             3.4%;  Score 66;  DB 8;  Length 2190;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-24;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
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Db       1476 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1535

Qy       1492 TCTGAG 1497
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Db       1536 TCTGAG 1541


RESULT 12
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LOCUS       AF370509                2257 bp    mRNA    linear   PLN 30-APR-2001
DEFINITION  Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
            complete cds.
ACCESSION   AF370509
VERSION     AF370509.1  GI:13877616
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2257)
  AUTHORS   Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     e-mail for correspondence: arab@sequence.stanford.edu

            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis  Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Southwick,A.,
            Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M., Palm,C.J.,
            Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
            Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
            Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

            Southwick,A. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
            equally to this work.  Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford) contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
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ORIGIN

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Db       1613 TCTGAG 1618


RESULT 13
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DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24.
ACCESSION   AB020746 BA000014
VERSION     AB020746.1  GI:3985949
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 3. II.
            Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
            and BAC clones
  JOURNAL   DNA Res. 7 (3), 217-221 (2000)
  MEDLINE   20363099
   PUBMED   10907853
REFERENCE   2  (bases 1 to 79706)
  AUTHORS   Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MOB24
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is MXP5 and the 3' clone is MSD24.
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                     6601. .6648,6743. .6776,6882. .7013,7464. .7559,7677. .7743,
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                     FLYKVVEDPDLLPRMMLEKERTKQQQQVSDKKKRRVTMSTVKSEEEEVEEDEGRVFRV
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RESULT 14
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DEFINITION  Arabidopsis thaliana clone 17909 mRNA, complete sequence.
ACCESSION   AY089024
VERSION     AY089024.1  GI:21407798
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 2324)
  AUTHORS   Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
            Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
  TITLE     Full-length messenger RNA sequences greatly improve genome
            annotation
  JOURNAL   Genome Biol. 3 (6), RESEARCH0029 (2002)
  MEDLINE   22088475
   PUBMED   12093376
REFERENCE   2  (bases 1 to 2324)
  AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
            Feldmann,K.
  TITLE     Full-Length cDNA from Arabidopsis thaliana
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2324)
  AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
            Feldmann,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
            Malibu, CA 90265, USA
COMMENT     This clone sequence is one of 5,000 Ceres full-length cDNAs made
            available to TIGR and Genbank. The following quality assessment of
            this set was done by comparison with known proteins: two percent of
            the clones are estimated to be 5'-truncated; less than one percent
            are 3'-truncated; approximately two percent represent alternative
            splice variants, including unspliced introns and spliced exons; one
            percent may contain premature stop codons; five percent may have
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frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-13;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1585 GCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 1631
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RESULT 15
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DEFINITION  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K7M2.
ACCESSION   AP000382 BA000014
VERSION     AP000382.1  GI:5672513
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
  TITLE     Structural analysis of Arabidopsis thaliana chromosome 3. II.
            Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
            and BAC clones
  JOURNAL   DNA Res. 7 (3), 217-221 (2000)
  MEDLINE   20363099
   PUBMED   10907853
REFERENCE   2  (bases 1 to 80393)
  AUTHORS   Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Yasukazu Nakamura, Kazusa DNA Research
            Institute, Department of Plant Gene Research; 1532-3, Yana,
            Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
            Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT     Address for correspondence: kaos@kazusa.or.jp
            For the latest information on annotation of this clone, please see
            http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K7M2
            Genes with similarity to proteins in the databases are described in
            'product' or 'note' qualifiers.  Genes that have no significant
            protein similarity are described as 'unknown protein'.
            The software programs used to predict genes include: Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/Grail-1.3/),
            GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
            NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
            SplicePredictor (Volker Brendel, Stanford University,
            http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
            Genes encoding tRNAs are predicted by tRNAscan-SE
            (Sean Eddy, Washington University School of Medicine, St. Louis,
            http://genome.wustl.edu/eddy/tRNAscan-SE/).
            This sequence may not be the entire insert of this clone. It may be
            shorter because we remove overlaps between neighboring submissions.
            The 5' clone is K13K6 and the 3' clone is MXP5.

FEATURES             Location/Qualifiers
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Query Match 1.5%; Score 29; DB 8; Length 80393;
Best Local Similarity 100.0%; Pred. No. 0.001;
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Job time : 7366 secs

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OM nucleic - nucleic search, using sw model

Run on: May 12, 2004, 11:40:28 ; Search time 742 Seconds
(without alignments)
11130.050 Million cell updates/sec

Title: US-10-086-464-1
Perfect score: 1944
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1944	100.0	1944	4	AAF77094	Aaf77094 Brassica
	2	1944	100.0	1944	9	ACF36548	Acf36548 B. napus
	3	1944	100.0	2189	9	ACF36549	Acf36549 B. napus
	4	66	3.4	1959	9	ACF36557	Acf36557 A. thalia
	5	47	2.4	2324	3	AAC36968	Aac36968 Arabidops
	6	26	1.3	1515	9	ACF36555	Acf36555 Z. mays P
c	7	26	1.3	110000	3	AAF22305_06	Continuation (7 of
c	8	26	1.3	110000	3	AAF22305_07	Continuation (8 of
c	9	24	1.2	1389	7	ADA70853	Ada70853 Rice gene
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	18	23	1.2	1281	7	AAD47599	Aad47599 Human HGF
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	42	20	1.0	609	4	AAF97928	Aaf97928 Human sec
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ALIGNMENTS

RESULT 1
AAF77094
ID AAF77094 standard; DNA; 1944 BP.
XX
AC AAF77094;
XX
DT 17-MAY-2001 (first entry)
XX
DE Brassica napus PERK1 DNA.
XX
KW Proline-rich extensin-like receptor kinase; PERK; resistance; plant; ds.
XX
OS Brassica napus.
XX
PN WO200114563-A1.
XX
PD 01-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-CA000966.
XX
PR 19-AUG-1999; 99US-0149466P.
PR 13-OCT-1999; 99US-0159122P.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
XX
PI Goring D, Silva N;
XX
DR WPI; 2001-244305/25.
XX
PT New proline-rich, extensin-like receptor kinase nucleic acids and
PT polypeptides useful for increasing plant wounding or pathogen resistance,
PT or for producing transgenic plants with increased wounding or pathogen
PT resistance.
XX
PS Claim 6; Fig 1; 91pp; English.
XX
CC The present invention relates to proline-rich extensin-like receptor
CC kinase (PERK). The PERK nucleic acids and polypeptides are useful for
CC increasing the resistance of plants to wounding and pathogens. These are
CC also useful for producing transgenic plants with increased wounding and
CC pathogen resistance compared with a wild type plant, as well as in assays
CC for identifying and developing compounds to inhibit and/or enhance
CC polypeptide function directly
XX
SQ Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 1944; DB 4; Length 1944;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
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Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
              |||||||||||||||||||||||||
Db       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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RESULT 2
ACF36548
ID ACF36548 standard; cDNA; 1944 BP.
XX
AC ACF36548;
XX
DT 18-DEC-2003 (first entry)
XX

```
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
FH   Key             Location/Qualifiers
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FT                   /transl_except= (pos: 1332. .1334, aa: Phe)
FT                   /product= "PERK1"
FT                   /note= "Proline-rich Extensin-like Receptor Kinase"
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PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Claim 3; Fig 1A; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 1944 BP; 464 A; 550 C; 459 G; 471 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1944;  DB 9;  Length 1944;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1944;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

Qy         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120

Qy        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180

Qy        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240

Qy        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300

Qy        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360

Qy        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480
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Db        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660

Qy        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

Qy        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900

Qy        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

Qy        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140
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Db       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200
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Db       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200

Qy       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260
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Db       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
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Db       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
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Qy       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
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Db       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500
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Db       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
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Db       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
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Db       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
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Db       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800
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Db       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
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Db       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920
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Db       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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Db       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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```
RESULT 3
ACF36549
ID   ACF36549 standard; cDNA; 2189 BP.
XX
AC   ACF36549;
XX
DT   18-DEC-2003  (first entry)
XX
DE   B. napus PERK1 receptor kinase encoding cDNA.
XX
KW   PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW   wound; pathogen resistance; plant growth; seed production; gene; ss.
XX
OS   Brassica napus.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  c
FT                   /note= "ABR82938; this protein contains the amino acids
FT                   corresponding to 5' and 3'UTR regions, though only the
FT                   relevant aa residues (ABR82937) is used in the invention"
FT   5'UTR           1. .96
FT                   /*tag=  a
FT   CDS             97. .2040
FT                   /*tag=  b
FT                   /transl_except= (pos: 1332. .1334, aa: Phe)
FT                   /product= "PERK1"
FT                   /note= "ABR82937; proline-rich Extensin-like Receptor
FT                   Kinase"
FT   3'UTR           2041. .2189
FT                   /*tag=  d
XX
PN   WO2003072763-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-CA000274.
XX
PR   28-FEB-2002; 2002CA-02373903.
PR   28-FEB-2002; 2002US-00086464.
XX
PA   (GORI/) GORING D.
PA   (SILV/) SILVA N.
PA   (HAFF/) HAFFANI Y Z.
XX
PI   Goring D,  Silva N,  Haffani YZ;
XX
DR   WPI; 2003-712727/67.
DR   P-PSDB; ABR82937, ABR82938.
XX
PT   Producing a transgenic plant having an increased plant resistance, plant
PT   growth or seed production comprises transforming a plant with a nucleic
PT   acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT   activity.
XX
PS   Disclosure; Fig 1D; 123pp; English.
XX
CC   The invention relates to producing a transgenic plant having increased
CC   plant height, number of branches, number of seed pods and/or seed
CC   production compared to a non-transgenic plant, and/or quicker flowering
CC   or later senescence compared to a non-transgenic plant. The method
CC   involves transforming a plant with a vector including a Proline-rich
CC   Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC   acid molecule having PERK activity. The method, as well as the PERK
CC   nucleic acid molecule and polypeptide, are useful in increasing plant
CC   resistance to wounding and pathogens and in increasing plant growth and
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a cDNA encoding a B. napus PERK1 receptor kinase
CC   polypeptide
XX
SQ   Sequence 2189 BP; 544 A; 592 C; 494 G; 559 T; 0 U; 0 Other;
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  Query Match            100.0%;  Score 1944;  DB 9;  Length 2189;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1944;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60
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Db         97 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 156

Qy         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 276

Qy        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 336

Qy        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456
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Qy       361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420
Db       457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy       421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480
Db       517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy       481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540
Db       577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy       541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
Db       637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy       601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660
Db       697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy       661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720
Db       757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy       721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780
Db       817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy       781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840
Db       877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy       841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900
Db       937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy       901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960
Db       997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy       961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
Db      1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy      1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080
Db      1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy      1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140
Db      1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy      1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200
Db      1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy      1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260
Db      1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy      1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
Db      1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy      1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
Db      1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy      1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
Db      1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy      1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500
Db      1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy      1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
Db      1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656

Qy      1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
Db      1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy      1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
Db      1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy      1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740
Db      1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy      1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800
Db      1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy      1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
Db      1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy      1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920
Db      1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy      1921 GGTTATAGTGGACCTTCTCTTTAA 1944
Db      2017 GGTTATAGTGGACCTTCTCTTTAA 2040
```

RESULT 4
ACF36557
ID ACF36557 standard; DNA; 1959 BP.
XX
AC ACF36557;
XX
DT 18-DEC-2003 (first entry)
XX
DE A. thaliana PERK1 protein encoding genomic DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.

XX
PS Disclosure; Fig 21d; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and
CC seed production. The nucleic acid molecule and polypeptide may also be
CC used in producing transgenic plants or transgenic host cells. The present
CC sequence represents an A. thaliana PERK1 DNA (At3g24550)
XX
SQ Sequence 1959 BP; 496 A; 514 C; 425 G; 524 T; 0 U; 0 Other;

Query Match 3.4%; Score 66; DB 9; Length 1959;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1432 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1491
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1447 AACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCA 1506

Qy 1492 TCTGAG 1497
||||||
Db 1507 TCTGAG 1512

RESULT 5
AAC36968
ID AAC36968 standard; DNA; 2324 BP.
XX
AC AAC36968;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15710.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 18-OCT-1999; 99US-0159584P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 2.4%; Score 47; DB 3; Length 2324;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1585 GCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 1631
||||||||||||||||||||||||||||||||||||||||||||||||
Db 1700 GCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 1746

RESULT 6
ACF36555
ID ACF36555 standard; DNA; 1515 BP.
XX
AC ACF36555;
XX
DT 18-DEC-2003 (first entry)
XX
DE Z. mays PERK protein encoding genomic DNA.
XX
KW PERK1; transgenic; plant; proline-rich extensin-like receptor kinase;
KW wound; pathogen resistance; plant growth; seed production; maize; gene;
KW ds.
XX
OS Zea mays.
XX
PN WO2003072763-A1.
XX
PD 04-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-CA000274.
XX
PR 28-FEB-2002; 2002CA-02373903.
PR 28-FEB-2002; 2002US-00086464.
XX
PA (GORI/) GORING D.
PA (SILV/) SILVA N.
PA (HAFF/) HAFFANI Y Z.
XX
PI Goring D, Silva N, Haffani YZ;
XX
DR WPI; 2003-712727/67.
XX
PT Producing a transgenic plant having an increased plant resistance, plant
PT growth or seed production comprises transforming a plant with a nucleic
PT acid molecule having a Proline-rich Extensin-like Receptor Kinase
PT activity.
XX
PS Disclosure; Fig 21b; 123pp; English.
XX
CC The invention relates to producing a transgenic plant having increased
CC plant height, number of branches, number of seed pods and/or seed
CC production compared to a non-transgenic plant, and/or quicker flowering
CC or later senescence compared to a non-transgenic plant. The method
CC involves transforming a plant with a vector including a Proline-rich
CC Extensin-like Receptor Kinase (PERK) nucleic acid molecule or a nucleic
CC acid molecule having PERK activity. The method, as well as the PERK
CC nucleic acid molecule and polypeptide, are useful in increasing plant
CC resistance to wounding and pathogens and in increasing plant growth and

```
CC   seed production. The nucleic acid molecule and polypeptide may also be
CC   used in producing transgenic plants or transgenic host cells. The present
CC   sequence represents a Z. mays PERK protein encoding genomic DNA (TIGR
CC   Accession No. AY108241)
XX
SQ   Sequence 1515 BP; 400 A; 330 C; 381 G; 404 T; 0 U; 0 Other;

  Query Match             1.3%;  Score 26;  DB 9;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
             ||||||||||||||||||||||||||
Db        601 TTTGAAGCTAAGGTTGCTGATTTTGG 626


RESULT 7
AAF22305_06/c
Continuation (7 of 11) of AAF22305 from base 600001 (Arabidopsis thaliana chromosome 4 c
WP Sequence split into 11 fragments  LOCUS AAF22305 Accession Aaf22305
WP     Fragment Name      Begin     End
WP     AAF22305_00            1    110000
WP     AAF22305_01       100001    210000
WP     AAF22305_02       200001    310000
WP     AAF22305_03       300001    410000
WP     AAF22305_04       400001    510000
WP     AAF22305_05       500001    610000
WP     AAF22305_06       600001    710000
WP     AAF22305_07       700001    810000
WP     AAF22305_08       800001    910000
WP     AAF22305_09       900001   1010000
WP     AAF22305_10      1000001   1082138

  Query Match             1.3%;  Score 26;  DB 3;  Length 110000;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1036 CTTGTCTATGAGTTTGTTCCTAACAA 1061
             ||||||||||||||||||||||||||
Db     109643 CTTGTCTATGAGTTTGTTCCTAACAA 109618


RESULT 8
AAF22305_07/c
Continuation (8 of 11) of AAF22305 from base 700001 (Arabidopsis thaliana chromosome 4 c
WP Sequence split into 11 fragments  LOCUS AAF22305 Accession Aaf22305
WP     Fragment Name      Begin     End
WP     AAF22305_00            1    110000
WP     AAF22305_01       100001    210000
WP     AAF22305_02       200001    310000
WP     AAF22305_03       300001    410000
WP     AAF22305_04       400001    510000
WP     AAF22305_05       500001    610000
WP     AAF22305_06       600001    710000
WP     AAF22305_07       700001    810000
WP     AAF22305_08       800001    910000
WP     AAF22305_09       900001   1010000
WP     AAF22305_10      1000001   1082138

  Query Match             1.3%;  Score 26;  DB 3;  Length 110000;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1036 CTTGTCTATGAGTTTGTTCCTAACAA 1061
             ||||||||||||||||||||||||||
Db       9643 CTTGTCTATGAGTTTGTTCCTAACAA 9618


RESULT 9
ADA70853/c
ID   ADA70853 standard; DNA; 1389 BP.
XX
AC   ADA70853;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene, SEQ ID 4176.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; rice;
KW   gene; ds.
XX
OS   Oryza sativa.
XX
PN   WO2003000898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H,  Chen W,  Cooper B,  Glazebrook J,  Goff SA,  Hou Y;
PI   Katagiri F,  Quan S,  Tao Y,  Whitham S,  Xie Z,  Zhu T,  Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 6; SEQ ID NO 4176; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1
CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 1389 BP; 412 A; 278 C; 406 G; 293 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 24;  DB 7;  Length 1389;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        670 CCTCCTCCACCTCCACCACCGCCT 693
              ||||||||||||||||||||||||
Db        115 CCTCCTCCACCTCCACCACCGCCT 92


RESULT 10
ADA27371
ID   ADA27371 standard; DNA; 1515 BP.
XX
AC   ADA27371;
XX
DT   20-NOV-2003  (first entry)
XX
DE   HPV-16 L1 codon optimised DNA sequence SEQ ID NO:1.
XX
KW   cell line; American Type Culture Collection PTA-4047; ATCC-4047;
KW   baculoviruses; viral recombinant protein; virus-like particle; vaccine;
KW   diagnostic reagent; human papillomavirus type 16; HPV-16; L1; gene; ds.
XX
OS   Synthetic.
OS   Human papillomavirus type 16.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1515
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FT                   /*tag=  a
FT                   /product= "HPV-16 L1 protein"
FT                   /transl_except= (pos:208. .210,aa:Tyr)
FT                   /transl_except= (pos:295. .297,aa:Val)
XX
PN   WO2003068804-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004516.
XX
PR   14-FEB-2002; 2002US-0356113P.
PR   14-FEB-2002; 2002US-0356118P.
PR   14-FEB-2002; 2002US-0356119P.
PR   14-FEB-2002; 2002US-0356123P.
PR   14-FEB-2002; 2002US-0356126P.
PR   14-FEB-2002; 2002US-0356133P.
PR   14-FEB-2002; 2002US-0356135P.
PR   14-FEB-2002; 2002US-0356150P.
PR   14-FEB-2002; 2002US-0356151P.
PR   14-FEB-2002; 2002US-0356152P.
PR   14-FEB-2002; 2002US-0356154P.
PR   14-FEB-2002; 2002US-0356156P.
PR   14-FEB-2002; 2002US-0356157P.
PR   14-FEB-2002; 2002US-0356161P.
PR   14-FEB-2002; 2002US-0356162P.
XX
PA   (NOVA-) NOVAVAX INC.
XX
PI   Robinson RA;
XX
DR   WPI; 2003-646475/61.
DR   P-PSDB; ADA27363.
XX
PT   New insect cell line designated ATCC PTA-4047, useful for replicating
PT   baculoviruses to produce large amounts of recombinant proteins of
PT   medical, pharmaceutical and veterinary importance.
XX
PS   Claim 10; Fig 1; 63pp; English.
XX
CC   The present invention describes a cell line comprising a cell that is a
CC   clone, derivative, mutant and/or transfectant of a cell line designated
CC   American Type Culture Collection (ATCC) PTA-4047. The cell upon culture
CC   grows continuously and retains the identifying characteristics of the
CC   cell line designated ATCC-4047. Also described is a process of making a
CC   cell line. The insect cell line is useful in replicating baculoviruses,
CC   as a host substrate for baculovirus plaque assays, as a source of insect
CC   proteins, acts as a depot for cell transfection to produce recombinant
CC   baculoviruses, and in expressing viral recombinant proteins.
CC   Extracellular and intracellular viral recombinant proteins and virus-like
CC   particles expressed from the cell line are useful as pharmaceutical
CC   compositions, vaccines or diagnostic reagents. The present sequence
CC   represents a human papillomavirus type 16 (HPV-16) L1 codon optimised
CC   sequence, which is used in the exemplification of the present invention.
XX
SQ   Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 24;  DB 8;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
              ||||||||||||||||||||||||
Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 11
ADA92549
ID   ADA92549 standard; DNA; 1515 BP.
XX
AC   ADA92549;
XX
DT   20-NOV-2003  (first entry)
XX
DE   HPV-16 L1 codon optimised DNA sequence SEQ ID NO:1.
XX
KW   codon optimised; viral capsid protein; virus-like particle; VLP;
KW   antigenic; human papillomavirus infection; virucide; vaccine;
KW   gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;
KW   L1; gene; ds.
XX
OS   Synthetic.
OS   Human papillomavirus type 16.
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FH   Key             Location/Qualifiers
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FT                   /product= "codon optimised L1 amino acid sequence"
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FT                   /transl_except= (pos:295. .297,aa:Val)
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PN   WO2003068933-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004480.
XX
PR   14-FEB-2002; 2002US-0356113P.
PR   14-FEB-2002; 2002US-0356118P.
PR   14-FEB-2002; 2002US-0356119P.
PR   14-FEB-2002; 2002US-0356123P.
PR   14-FEB-2002; 2002US-0356126P.
PR   14-FEB-2002; 2002US-0356133P.
PR   14-FEB-2002; 2002US-0356135P.
PR   14-FEB-2002; 2002US-0356150P.
PR   14-FEB-2002; 2002US-0356151P.
PR   14-FEB-2002; 2002US-0356152P.
PR   14-FEB-2002; 2002US-0356154P.
PR   14-FEB-2002; 2002US-0356156P.
PR   14-FEB-2002; 2002US-0356157P.
PR   14-FEB-2002; 2002US-0356161P.
PR   14-FEB-2002; 2002US-0356162P.
XX
PA   (NOVA-) NOVAVAX INC.
XX
PI   Robinson RA;
XX
DR   WPI; 2003-689664/65.
DR   P-PSDB; ADA92541.
XX
PT   New codon optimized polynucleotide encoding a viral capsid protein that
PT   self assembles into a virus-like particle, useful for diagnosing,
PT   preventing or treating human papillomavirus infections or associated
PT   disorders.
XX
PS   Claim 7; Page 113; 123pp; English.
XX
CC   The present invention describes a codon optimised polynucleotide encoding
CC   a viral capsid protein that self assembles into a virus-like particle
CC   (VLP) that exhibits conformational antigenic epitopes capable of raising
CC   neutralising antibodies, where the VLP is expressed from a host cell
CC   extracellularly. Also described: (1) a vector comprising the above codon
CC   optimised polynucleotide operably liked to a eukaryotic or prokaryotic
CC   regulatory control element, capable of replication in prokaryotic and/or
CC   eukaryotic host; (2) a host cell comprising the vector; (3) a
CC   pharmaceutical or vaccine composition for treating, ameliorating or
CC   preventing a papillomavirus related disease or disorder, comprising a
CC   multiplicity of VLPs that exhibit conformational antigenic epitopes, and
CC   a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a
CC   papillomavirus infection, comprising a multiplicity of VLPs that exhibit
CC   conformational antigenic epitopes, and a detection agent comprising a
CC   detectable label; (5) a method for preparing the above codon optimised
CC   polynucleotide, comprising replacing codons that are underutilised in
CC   insect cells with codons that are utilised at high levels in insect
CC   cells, to create an initially-modified nucleotide sequence, and modifying
CC   the initially-modified nucleotide sequence by choosing a preferred codon
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CC   for the initially-modified sequence, where the ratio of GC nucleotide
CC   pairs to AT nucleotide pairs in the further-modified nucleotide sequence
CC   trends towards about 1:1, where the number of palindromic and stem-loop
CC   DNA structures in the further-modified nucleotide sequence is minimised,
CC   and where the number of transcription and post-transcription repressor
CC   elements are minimised; and (6) methods for treating, ameliorating or
CC   preventing a papillomavirus related disease or disorder, or for
CC   protecting an individual against a papillomavirus infection, comprising
CC   administering to an individual an amount of the composition or vaccine
CC   cited above. The VLP has virucide activity and can be used in vaccines
CC   and in gene therapy. The composition and methods of the present invention
CC   are useful in diagnosing, preventing or treating human papillomavirus
CC   infections or associated disorders, such as dysplasia. The present
CC   sequence represents an HPV-16 codon optimised L1 nucleotide sequence from
CC   the present invention.
XX
SQ   Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 24;  DB 8;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
              ||||||||||||||||||||||||
Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 12
ADA14298
ID   ADA14298 standard; DNA; 1515 BP.
XX
AC   ADA14298;
XX
DT   06-NOV-2003  (first entry)
XX
DE   HPV-16 L1 codon optimised sequence SEQ ID NO:1.
XX
KW   purification; recombinant extracellular virus-like particle;
KW   recombinant intracellular virus-like particle; virus-like particle; VLP;
KW   virucide; vaccine; gene therapy; human papillomavirus; HPV; infection;
KW   dysplasia; HPV-16; L1; codon optimised; gene; ds.
XX
OS   Human papillomavirus type 16.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1515
FT                   /*tag=  a
FT                   /product= "HPV-16 L1 protein"
FT                   /transl_except= (pos:208. .210,aa:Tyr)
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XX
PN   WO2003068993-A1.
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PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004474.
XX
PR   14-FEB-2002; 2002US-0356113P.
PR   14-FEB-2002; 2002US-0356118P.
PR   14-FEB-2002; 2002US-0356119P.
PR   14-FEB-2002; 2002US-0356123P.
PR   14-FEB-2002; 2002US-0356126P.
PR   14-FEB-2002; 2002US-0356133P.
PR   14-FEB-2002; 2002US-0356135P.
PR   14-FEB-2002; 2002US-0356150P.
PR   14-FEB-2002; 2002US-0356151P.
PR   14-FEB-2002; 2002US-0356152P.
PR   14-FEB-2002; 2002US-0356154P.
PR   14-FEB-2002; 2002US-0356156P.
PR   14-FEB-2002; 2002US-0356157P.
PR   14-FEB-2002; 2002US-0356161P.
PR   14-FEB-2002; 2002US-0356162P.
XX
PA   (NOVA-) NOVAVAX INC.
XX
PI   Robinson RA,  Thompson MW;
XX
DR   WPI; 2003-679645/64.
DR   P-PSDB; ADA14290.
XX
PT   Purifying a recombinant human papillomavirus (HPV) L1, useful for
PT   diagnosing, preventing or treating HPV infections, comprises clarifying,
PT   concentrating and diafiltering cells containing HPV particles.
XX
PS   Example 4; Fig 1A-C; 111pp; English.
XX
CC   The present invention describes a method for purifying a recombinant
CC   extracellular or intracellular virus-like particle (VLP). The method
CC   comprises harvesting a cell suspension comprising cells containing a
CC   plurality of VLPs to produce a harvested supernatant, optionally
CC   disrupting the harvested cells to produce cell lysates containing the
CC   VLP, clarifying the harvested supernatant, concentrating the clarified
CC   supernatant, diafiltering the concentrated supernatant, and recovering
CC   the purified recombinant VLP. Also described: (1) a cell line designated
CC   as Sf-9S deposited as American Type Culture Collection (ATCC) PTA-4047;
CC   (2) producing the cell line described above; (3) host cells that express
CC   one or more recombinant gene products with an enhanced yield; (4)
CC   producing a foreign protein in an insect cell; (5) nucleic acid sequences
CC   that correspond to and code for human papillomavirus (HPV) polypeptides;
CC   and (6) pharmaceutical compositions comprising an amount of the
CC   recombinant viral gene products, VLPs, agonists, antagonists, or the
CC   active fragment of a viral gene product. The VLPs have virucide activity,
CC   and can be used in vaccines and in gene therapy. The method is useful in
CC   isolating and purifying expressed viral gene products, including VLPs, in
CC   vitro. The gene products or particles may be used in detecting,
CC   preventing or treating HPV infections and associated symptoms like
CC   dysplasia. The present sequence represents an HPV-16 L1 codon optimised
CC   nucleotide sequence, which is given in the exemplification of the present
CC   invention.
XX
SQ   Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 24;  DB 8;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
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Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 13
AAD58571
ID   AAD58571 standard; DNA; 1515 BP.
XX
AC   AAD58571;
XX
DT   04-DEC-2003  (first entry)
XX
DE   HPV-16 L1 codon optimised DNA.
XX
KW   Vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV;
KW   virucide; papillomavirus infection; gene; Human papillomavirus; ds.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1515
FT                   /*tag=  a
FT                   /product= "HPV-16 L1 protein"
FT                   /transl_except= (pos:208. .210, aa:Tyr)
FT                   /transl_except= (pos:295. .297, aa:Val)
FT                   /note= "No stop codon"
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PN   WO2003068163-A2.
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PF   14-FEB-2003; 2003WO-US004473.
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PR   14-FEB-2002; 2002US-0356113P.
PR   14-FEB-2002; 2002US-0356118P.
PR   14-FEB-2002; 2002US-0356119P.
PR   14-FEB-2002; 2002US-0356123P.
PR   14-FEB-2002; 2002US-0356126P.
PR   14-FEB-2002; 2002US-0356133P.
PR   14-FEB-2002; 2002US-0356135P.
PR   14-FEB-2002; 2002US-0356150P.
PR   14-FEB-2002; 2002US-0356151P.
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PR   14-FEB-2002; 2002US-0356161P.
PR   14-FEB-2002; 2002US-0356162P.
XX
PA   (NOVA-) NOVAVAX INC.
XX
PI   Robinson RA,  Cioce V;
XX
DR   WPI; 2003-689598/65.
DR   P-PSDB; AAE38615.
XX
PT   New chimeric virus-like particles comprising a recombinant viral capsid
PT   protein encapsulating a recombinant viral protein, useful for inducing
PT   humoral and/or cell-mediated immunity against papillomavirus infection.
XX
PS   Claim 10; Fig 1A-1C; 126pp; English.
XX
CC   The present invention relates to chimeric virus-like particle comprising
CC   a recombinant viral capsid protein that encapsulates a recombinant viral
CC   protein during self assembly into a chimeric virus-like particle and
CC   exhibiting conformational antigenic epitopes capable of eliciting
CC   neutralising antibodies. The vaccine comprising the chimeric virus-like
CC   particles are useful for inducing immunity (humoral and/or cell-mediated
CC   immunity) against papillomavirus infection. The invention is also useful
CC   in gene therapy. The present sequence is HPV (human papillomavirus)-16 L1
CC   codon optimised DNA
XX
SQ   Sequence 1515 BP; 297 A; 632 C; 308 G; 278 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 24;  DB 8;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
              ||||||||||||||||||||||||
Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 14
AAD47597
ID   AAD47597 standard; DNA; 897 BP.
XX
AC   AAD47597;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human HGFR M1250T mutant DNA fragment.
XX
KW   Human; hepatocyte growth factor receptor kinase; hHGFR; proto-oncogene;
KW   protein co-ordinate data; drug design; hepatocyte growth factor; tumour;
KW   therapy; enzyme; mutant; gene; ds.
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OS   Synthetic.
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PN   EP1243596-A2.
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PD   25-SEP-2002.
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PF   25-MAR-2002; 2002EP-00006616.
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PR   23-MAR-2001; 2001US-0277968P.
XX
PA   (AGOU-) AGOURON PHARM INC.
XX
PI   Mroczkowski B,  Hickey M,  Mctigue MA,  Murray BW,  Parge H,  Sarup J;
PI   Zhu J;
XX
DR   WPI; 2003-001650/01.
DR   P-PSDB; AAE30097.
XX
PT   New polynucleotide encoding human hepatocyte growth factor receptor,
PT   useful for designing modulators of the receptor, and potential antitumor
PT   agents.
XX
PS   Claim 4; Page 157; 204pp; English.
XX
CC   The invention relates to human hepatocyte growth factor receptor kinase
CC   (hHGFR) and its nucleic acid sequence. The invention also relates to
CC   methods for identification of hHGFR inhibitors. hHGFR DNA is used to
CC   express the corresponding polypeptides and these are used to provide
CC   protein co-ordinate data useful in rational drug design of compounds that
CC   modulate kinase domain, potentially useful for treating diseases
CC   associated with signalling between hHGFR and hepatocyte growth factor,
CC   particularly tumours (since HGFR is a proto-oncogene). It can also be
CC   used to search databases for related sequences and its fragments as
CC   primers or probes. The present sequence is human HGFR mutant DNA fragment
CC   used to illustrate the method of the invention
XX
SQ   Sequence 897 BP; 257 A; 193 C; 207 G; 240 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 23;  DB 7;  Length 897;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 AAGGTTGCTGATTTTGGTCTTGC 1262
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Db        508 AAGGTTGCTGATTTTGGTCTTGC 530


RESULT 15
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ID   AAD47600 standard; DNA; 897 BP.
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AC   AAD47600;
XX
DT   24-FEB-2003  (first entry)
XX
DE   Human HGFR H1094R mutant DNA fragment.
XX
KW   Human; hepatocyte growth factor receptor kinase; hHGFR; proto-oncogene;
KW   protein co-ordinate data; drug design; hepatocyte growth factor; tumour;
KW   therapy; enzyme; mutant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .897
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FT                   /product= "Human HGFR mutant protein fragment"
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PN   EP1243596-A2.
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PD   25-SEP-2002.
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PF   25-MAR-2002; 2002EP-00006616.
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PR   23-MAR-2001; 2001US-0277968P.
XX
PA   (AGOU-) AGOURON PHARM INC.
XX
PI   Mroczkowski B,  Hickey M,  Mctigue MA,  Murray BW,  Parge H,  Sarup J;
PI   Zhu J;
XX
DR   WPI; 2003-001650/01.
DR   P-PSDB; AAE30100.
XX
PT   New polynucleotide encoding human hepatocyte growth factor receptor,
PT   useful for designing modulators of the receptor, and potential antitumor
PT   agents.
XX
PS   Claim 6; Page 160-161; 204pp; English.
XX
CC   The invention relates to human hepatocyte growth factor receptor kinase
CC   (hHGFR) and its nucleic acid sequence. The invention also relates to
CC   methods for identification of hHGFR inhibitors. hHGFR DNA is used to
CC   express the corresponding polypeptides and these are used to provide
CC   protein co-ordinate data useful in rational drug design of compounds that
CC   modulate kinase domain, potentially useful for treating diseases
CC   associated with signalling between hHGFR and hepatocyte growth factor,
CC   particularly tumours (since HGFR is a proto-oncogene). It can also be
CC   used to search databases for related sequences and its fragments as
CC   primers or probes. The present sequence is human HGFR mutant DNA fragment
CC   used to illustrate the method of the invention
XX
SQ   Sequence 897 BP; 257 A; 191 C; 209 G; 240 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 23;  DB 7;  Length 897;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 AAGGTTGCTGATTTTGGTCTTGC 1262
              |||||||||||||||||||||||
Db        508 AAGGTTGCTGATTTTGGTCTTGC 530


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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	65	3.3	314	14	CD811645	CD811645 BN10.001E
5	65	3.3	314	14	CD811912	CD811912 BN10.019G
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c 7	53	2.7	584	9	AV543493	AV543493 AV543493
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43	26	1.3	673	14	CA164704	CA164704 SCSBRZ312
44	26	1.3	682	13	CA095337	CA095337 SCCCCL500
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ALIGNMENTS

RESULT 1
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DEFINITION RFO2.114I04F010529 RFO2 Brassica napus cDNA clone RFO2114I04, mRNA sequence.
ACCESSION CD839231
VERSION CD839231.1 GI:32521171
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 723)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .723

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ORIGIN

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Qy       1534 AATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTT 1593
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Db        191 AATAATGGGTATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTT 250

Qy       1594 CGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATTGTGCGTGCGTTAGAAGGAAAT 1653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 CGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGATTGTGCGTGCGTTAGAAGGAAAT 310

Qy       1654 GTATCACTGTCAGATCTTAACGAAGGGATGAGACCAGGTCAAAGCAATGTATACAGCTCA 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 GTATCACTGTCAGATCTTAACGAAGGGATGAGACCAGGTCAAAGCAATGTATACAGCTCA 370

Qy       1714 TACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAGAAGTTTAGG 1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 TACGGAGGAAGCACCGATTATGACTCGAGCCAGTACAATGAAGACATGAAGAAGTTTAGG 430

Qy       1774 AAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAATCCGACCAGT 1833
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 AAAATGGCTCTTGGAACTCAAGAGTACAACGCCACGGGTGAGTACAGTAATCCGACCAGC 490

Qy       1834 GACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGCGAAATGGAG 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        491 GACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGCGAAATGGAG 550

Qy       1894 ATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCTTTAA 1944
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 ATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCTTTAA 601


RESULT 2
BH442220
LOCUS       BH442220                453 bp    DNA     linear   GSS 12-DEC-2001
DEFINITION  BOGLN68TR BOGL Brassica oleracea genomic clone BOGLN68, genomic
            survey sequence.
ACCESSION   BH442220
VERSION     BH442220.1  GI:17627934
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGLN68TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .453
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGLN68"
                     /clone_lib="BOGL"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             14.0%;  Score 273;  DB 28;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-112;
  Matches  273;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1627 CAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGGATGAGA 1686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 CAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGGATGAGA 228

Qy       1687 CCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAG 1746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 CCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCGAGCCAG 288

Qy       1747 TACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCC 1806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 TACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCC 348

Qy       1807 ACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGC 1866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGC 408

Qy       1867 GAGGGCCAAACCACACGCGAAATGGAGATGGGG 1899
             ||||||||||||||||||||||||||||||||
Db        409 GAGGGCCAAACCACACGCGAAATGGAGATGGGG 441


RESULT 3
BZ455058
LOCUS       BZ455058                753 bp    DNA     linear   GSS 13-DEC-2002
DEFINITION  BONKA33TF BO_1.6_2_KB_tot Brassica oleracea genomic clone BONKA33,
            genomic survey sequence.
ACCESSION   BZ455058
VERSION     BZ455058.1  GI:26731783
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BONKA33TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .753
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
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                     /db_xref="taxon:3712"
                     /clone="BONKA33"
                     /clone_lib="BO_1.6_2_KB_tot"
                     /note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             9.6%;  Score 187;  DB 28;  Length 753;
  Best Local Similarity   100.0%;  Pred. No. 2e-73;
  Matches  187;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1282 AACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCGGAATACGCT 1341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 AACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCGGAATACGCT 70

Qy       1342 GCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTGCTTTTGGAG 1401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 GCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTGCTTTTGGAG 130

Qy       1402 CTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTT 1461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 CTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTT 190

Qy       1462 GACTGGG 1468
              |||||||
Db        191 GACTGGG 197


RESULT 4
CD811645
LOCUS       CD811645                314 bp    mRNA    linear   EST 10-JUL-2003
DEFINITION  BN10.001E08F011207 BN10 Brassica napus cDNA clone BN10001E08, mRNA
            sequence.
ACCESSION   CD811645
VERSION     CD811645.1  GI:32493585
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .314
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN10001E08"
                     /tissue_type="seed"
                     /clone_lib="BN10"
ORIGIN

  Query Match             3.3%;  Score 65;  DB 14;  Length 314;
  Best Local Similarity   99.1%;  Pred. No. 3.8e-18;
  Matches  115;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1825 CCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 1884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 60

Qy       1885 GAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCT 1940
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCT 116


RESULT 5
CD811912
LOCUS       CD811912                314 bp    mRNA    linear   EST 10-JUL-2003
DEFINITION  BN10.019G03F020121 BN10 Brassica napus cDNA clone BN10019G03, mRNA
            sequence.
ACCESSION   CD811912
VERSION     CD811912.1  GI:32493852
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 314)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .314
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Jet neuf"
                     /db_xref="taxon:3708"
                     /clone="BN10019G03"
                     /tissue_type="seed"
                     /clone_lib="BN10"
ORIGIN

  Query Match             3.3%;  Score 65;  DB 14;  Length 314;
  Best Local Similarity   99.1%;  Pred. No. 3.8e-18;
  Matches  115;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1825 CCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 1884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGCCAAACCACACGC 60

Qy       1885 GAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCT 1940
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGATGGAGATGGGGAAGATTAAGAGAACCGGTCAGGGTTATAGTGGACCTTCTCT 116


RESULT 6
AV539333/c
LOCUS       AV539333                561 bp    mRNA    linear   EST 07-SEP-2000
DEFINITION  AV539333 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
            cDNA clone RZ130c07F 3', mRNA sequence.
ACCESSION   AV539333
VERSION     AV539333.1  GI:8701090
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 561)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
  JOURNAL   DNA Res. 7 (3), 175-180 (2000)
  MEDLINE   20363093
```

```
   PUBMED   10907847
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .561
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="RZ130c07F"
                     /tissue_type="roots"
                     /clone_lib="Arabidopsis thaliana roots Columbia"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             2.7%;  Score 53;  DB 9;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1579 GCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 1631
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 491


RESULT 7
AV543493/c
LOCUS       AV543493                584 bp    mRNA    linear   EST 07-SEP-2000
DEFINITION  AV543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
            cDNA clone RZ201f07F 3', mRNA sequence.
ACCESSION   AV543493
VERSION     AV543493.1  GI:8714907
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
  JOURNAL   DNA Res. 7 (3), 175-180 (2000)
  MEDLINE   20363093
   PUBMED   10907847
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .584
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="RZ201f07F"
                     /tissue_type="roots"
                     /clone_lib="Arabidopsis thaliana roots Columbia"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             2.7%;  Score 53;  DB 9;  Length 584;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-12;
  Matches   53;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1579 GCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 1631
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAGAT 416


RESULT 8
BH432371
LOCUS       BH432371                754 bp    DNA     linear   GSS 12-DEC-2001
DEFINITION  BOGVQ93TR BOGV Brassica oleracea genomic clone BOGVQ93, genomic
            survey sequence.
ACCESSION   BH432371
VERSION     BH432371.1  GI:17618092
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGVQ93TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .754
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGVQ93"
                     /clone_lib="BOGV"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             2.2%;  Score 42;  DB 28;  Length 754;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-07;
  Matches   42;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1762 AAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAAC 1803
             ||||||||||||||||||||||||||||||||||||||||||
Db        462 AAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAAC 503


RESULT 9
BZ456327
LOCUS       BZ456327                342 bp    DNA     linear   GSS 13-DEC-2002
DEFINITION  BONBB66TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONBB66,
            genomic survey sequence.
ACCESSION   BZ456327
VERSION     BZ456327.1  GI:26734454
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
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```
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .342
                      /organism="Brassica oleracea"
                      /mol_type="genomic DNA"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BONBB66"
                      /clone_lib="BO_1.6_2_KB_tot"
                      /note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
                      total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             1.6%;  Score 32;  DB 28;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 0.0038;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         37 CCATCTCCACCATCAAACTCCACAACCACCAC 68
              ||||||||||||||||||||||||||||||||
Db        182 CCATCTCCACCATCAAACTCCACAACCACCAC 213


RESULT 10
BZ066106/c
LOCUS       BZ066106                744 bp    DNA     linear   GSS 10-OCT-2002
DEFINITION  1jl70e12.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BZ066106
VERSION     BZ066106.1  GI:23679353
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 744)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: ljl70  row: e  column: 12
            Seq primer: -28RPpOT reverse
            Class: shotgun
            High quality sequence start: 17
            High quality sequence stop: 551.
FEATURES              Location/Qualifiers
     source           1. .744
                      /organism="Brassica oleracea"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:3712"
                      /clone_lib="B.oleracea002"
                      /note="Vector: pOTw13; Whole genome shotgun library from
                      flowering buds. DNA was purified  from a crude nuclear
                      prep using Brassica oleracea TO1000DH3 buds  provided by
                      Thosmas Osborn at the University of Wisconsin. Genomic
                      DNA was provided by Pablo Rabinowicz (CSHL) and the
                      shotgun library  prepared at Washington University Genome
                      Sequencing Center."
ORIGIN

  Query Match             1.5%;  Score 30;  DB 28;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1596 CCATTCAGCTCGCCGCAGACCTCGCATGAG 1625
              ||||||||||||||||||||||||||||||
Db        729 CCATTCAGCTCGCCGCAGACCTCGCATGAG 700


RESULT 11
BM061076
LOCUS       BM061076                505 bp    mRNA    linear   EST 11-SEP-2002
DEFINITION  KS01026B11 KS01 Capsicum annuum cDNA, mRNA sequence.
ACCESSION   BM061076
VERSION     BM061076.1  GI:22781194
KEYWORDS    EST.
SOURCE      Capsicum annuum
  ORGANISM  Capsicum annuum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Capsicum.
REFERENCE   1  (bases 1 to 505)
  AUTHORS   Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S.,
            Hur,C.-G. and Choi,D.
  TITLE     Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
            annuum L.) and Sequence Analysis in Relation to Hypersensitive
            Response Against Pathogen
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Doil Choi
            Genome Research Center and National Center for Genome Information
            Korea Research Institute of Bioscience and Biotechnology
            P.O. Box 115, Yusong, Taejeon, 305-600, Republic of Korea
            Tel: 82-42-860-4340
            Fax: 82-42-860-4309
            Email: doil@mail.kribb.re.kr
            High quality sequence stop: 505.
FEATURES              Location/Qualifiers
     source           1. .505
                      /organism="Capsicum annuum"
                      /mol_type="mRNA"
                      /cultivar="Bukang"
                      /db_xref="taxon:4072"
                      /tissue_type="leaf inoculated with Xanthomonas campestris
                      pv. glycines"
                      /dev_stage="8 weeks after germination"
                      /clone_lib="KS01"
                      /note="Vector: pBluescript SK(-)"
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  Best Local Similarity   100.0%;  Pred. No. 0.095;
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Qy       1244 TTGCTGATTTTGGTCTTGCTAAGATTGCT 1272
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Db         58 TTGCTGATTTTGGTCTTGCTAAGATTGCT 86


RESULT 12
AV551753
LOCUS       AV551753                573 bp    mRNA    linear   EST 06-SEP-2000
DEFINITION  AV551753 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
            cDNA clone RZ130c07R 5', mRNA sequence.
ACCESSION   AV551753
VERSION     AV551753.1  GI:8723166
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
  JOURNAL   DNA Res. 7 (3), 175-180 (2000)
  MEDLINE   20363093
   PUBMED   10907847
```

```
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="RZ130c07R"
                     /tissue_type="roots"
                     /clone_lib="Arabidopsis thaliana roots Columbia"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.099;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        880 TTGCCTAGTGGGAAAGAAGTTGCTGTGAA 908
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Db        471 TTGCCTAGTGGGAAAGAAGTTGCTGTGAA 499


RESULT 13
CC968148
LOCUS       CC968148                 607 bp    DNA     linear   GSS 18-AUG-2003
DEFINITION  BOIEB10TF BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
            BOIEB10, genomic survey sequence.
ACCESSION   CC968148
VERSION     CC968148.1  GI:33822075
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 607)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOIEB10TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .607
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOIEB10"
                     /clone_lib="BO_1.4_1.6_KB_nuc"
                     /note="Vector: pHOS2; Site_1: BstXI; 1.4-1.6 kb sheared
                     nuclear DNA inserted into pHOS2 using BstXI linkers"
ORIGIN

  Query Match             1.5%;  Score 29;  DB 29;  Length 607;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        871 AAAGGTGTGTTGCCTAGTGGGAAAGAAGT 899
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Db        431 AAAGGTGTGTTGCCTAGTGGGAAAGAAGT 459


RESULT 14
BH577077/c
LOCUS       BH577077                 620 bp    DNA     linear   GSS 14-DEC-2001
DEFINITION  BOHCX77TR BOHC Brassica oleracea genomic clone BOHCX77, genomic
            survey sequence.
ACCESSION   BH577077
VERSION     BH577077.1  GI:17829358
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHCX77TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHCX77"
                     /clone_lib="BOHC"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             1.5%;  Score 29;  DB 28;  Length 620;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        871 AAAGGTGTGTTGCCTAGTGGGAAAGAAGT 899
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Db        567 AAAGGTGTGTTGCCTAGTGGGAAAGAAGT 539


RESULT 15
BU043317
LOCUS       BU043317                 651 bp    mRNA    linear   EST 26-AUG-2002
DEFINITION  PP_LEa0015K13f Peach developing fruit mesocarp Prunus persica cDNA
            clone PP_LEa0015K13f, mRNA sequence.
ACCESSION   BU043317
VERSION     BU043317.1  GI:22483394
KEYWORDS    EST.
SOURCE      Prunus persica (peach)
  ORGANISM  Prunus persica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Callahan,A., Palmer,M., Main,D., Wing,R. and Abbott,A.
  TITLE     Peach Model Genome for Rosaceae
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Abbott, A.
            Dept of Genetics and Biochemistry
            Clemson University
            122 Long Hall, Clemson University, Clemson, SC 29634, USA
            Tel: 864 656 3060
            Fax: 864 656 6879
```

```
            Email: aalbert@clemson.edu
            Total High Quality bases = 578
            Seq primer: TAATACGACTCACTATAGGG
            High quality sequence stop: 651.
FEATURES              Location/Qualifiers
     source           1. .651
                      /organism="Prunus persica"
                      /mol_type="mRNA"
                      /cultivar="Loring"
                      /db_xref="taxon:3760"
                      /clone="PP_LEa0015K13f"
                      /tissue_type="Mesocarp"
                      /lab_host="E. coli"
                      /clone_lib="Peach developing fruit mesocarp"
                      /note="Vector: pBluescript II SK(-); Site_1: EcoRI;
                      Site_2: XhoI; authority=Prunus persica L. Batsh; The
                      sequence has been trimmed to remove vector sequence and
                      contains a minimum of 100 bases of phred value 20 or
                      above. For more details on library preparation and
                      sequence analysis go to
                      http://www.genome.clemson.edu/projects/peach. To order
                      this clone go to http://www.genome.clemson.edu/orders"
ORIGIN

  Query Match             1.5%;  Score 29;  DB 13;  Length 651;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        270 GAGATGGCTCGCATGGTTGCTTGTGCTGC 298


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	1.2	4626	1	US-08-306-691B-22	Sequence 22, Appl
2	23	1.2	4626	5	PCT-US93-06251-27	Sequence 27, Appl
3	20	1.0	609	4	US-09-800-729-55	Sequence 55, Appl
4	20	1.0	852	4	US-09-252-991A-1274	Sequence 1274, Ap
c 5	20	1.0	909	4	US-09-252-991A-1381	Sequence 1381, Ap
c 6	20	1.0	1092	4	US-09-252-991A-1287	Sequence 1287, Ap
7	20	1.0	3097	4	US-09-228-986-11	Sequence 11, Appl
8	20	1.0	5720	4	US-09-800-729-18	Sequence 18, Appl
c 9	20	1.0	41100	4	US-09-755-665-46	Sequence 46, Appl
10	19	1.0	358	3	US-08-991-789A-168	Sequence 168, App
11	19	1.0	358	4	US-09-062-451-168	Sequence 168, App
12	19	1.0	358	4	US-09-598-326-168	Sequence 168, App
13	19	1.0	358	4	US-09-289-198-168	Sequence 168, App
14	19	1.0	358	4	US-09-429-755-168	Sequence 168, App
c 15	19	1.0	2421	4	US-09-187-330-4	Sequence 4, Appli
c 16	19	1.0	2487	4	US-09-187-330-54	Sequence 54, Appl
c 17	19	1.0	3621	4	US-09-635-872A-21	Sequence 21, Appl
c 18	19	1.0	3621	4	US-09-636-077A-21	Sequence 21, Appl
c 19	19	1.0	3621	4	US-09-636-060C-21	Sequence 21, Appl
c 20	19	1.0	3621	4	US-09-986-552-21	Sequence 21, Appl
c 21	19	1.0	3783	4	US-09-635-872A-20	Sequence 20, Appl
c 22	19	1.0	3783	4	US-09-636-077A-20	Sequence 20, Appl
c 23	19	1.0	3783	4	US-09-636-060C-20	Sequence 20, Appl
c 24	19	1.0	3783	4	US-09-986-552-20	Sequence 20, Appl
25	19	1.0	5053	4	US-09-376-330-1	Sequence 1, Appli
c 26	19	1.0	5597	4	US-09-635-872A-4	Sequence 4, Appli
c 27	19	1.0	5597	4	US-09-636-077A-4	Sequence 4, Appli
c 28	19	1.0	5597	4	US-09-636-060C-4	Sequence 4, Appli
c 29	19	1.0	5597	4	US-09-986-552-4	Sequence 4, Appli
30	18	0.9	274	4	US-09-313-294A-2260	Sequence 2260, Ap
31	18	0.9	293	4	US-09-313-294A-6390	Sequence 6390, Ap
c 32	18	0.9	300	4	US-09-313-294A-4708	Sequence 4708, Ap
33	18	0.9	306	4	US-09-313-294A-4079	Sequence 4079, Ap
34	18	0.9	308	4	US-09-313-294A-5000	Sequence 5000, Ap
c 35	18	0.9	424	4	US-09-621-976-9270	Sequence 9270, Ap
c 36	18	0.9	439	4	US-09-397-787-273	Sequence 273, App
c 37	18	0.9	489	1	US-07-879-685B-3	Sequence 3, Appli
38	18	0.9	652	4	US-09-976-594-666	Sequence 666, App
c 39	18	0.9	657	4	US-09-833-381-921	Sequence 921, App
40	18	0.9	684	3	US-08-998-416-672	Sequence 672, App
41	18	0.9	1008	4	US-09-500-569-1	Sequence 1, Appli
42	18	0.9	1008	4	US-09-971-823B-1	Sequence 1, Appli
c 43	18	0.9	1276	3	US-09-177-325-2	Sequence 2, Appli
c 44	18	0.9	1276	3	US-09-411-812A-2	Sequence 2, Appli
c 45	18	0.9	1276	4	US-09-590-113-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-306-691B-22
; Sequence 22, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-306-691B-22

Query Match 1.2%; Score 23; DB 1; Length 4626;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1240 AAGGTTGCTGATTTTGGTCTTGC 1262

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Db       3903 AAGGTTGCTGATTTTGGTCTTGC 3925


RESULT 2
PCT-US93-06251-27
; Sequence 27, Application PC/TUS9306251
;  GENERAL INFORMATION:
;    APPLICANT:  Wickstrom, Eric and Rife, Jason P.
;    TITLE OF INVENTION:  Trivalent Synthesis of Oligonucleotides Containing
;    TITLE OF INVENTION:  Stereospecific Alkylphosphonates and Arylphosphonates
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCULLY, SCOTT, MURPHY & PRESSER
;      STREET:  400 Garden City Plaza
;      CITY:  Garden City
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  11530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06251
;      FILING DATE:  19930630
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DiGiglio, Frank S.
;      REGISTRATION NUMBER:  31,346
;      REFERENCE/DOCKET NUMBER:  8586
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-742-4343
;      TELEFAX:  516-742-4366
;      TELEX:  230 901 SANS UR
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4626 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US93-06251-27

  Query Match             1.2%;  Score 23;  DB 5;  Length 4626;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 AAGGTTGCTGATTTTGGTCTTGC 1262
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Db       3903 AAGGTTGCTGATTTTGGTCTTGC 3925


RESULT 3
US-09-800-729-55
; Sequence 55, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 55
;   LENGTH: 609
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (554)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-55

  Query Match             1.0%;  Score 20;  DB 4;  Length 609;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        667 CAACCTCCTCCACCTCCACC 686
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Db        269 CAACCTCCTCCACCTCCACC 288


RESULT 4
US-09-252-991A-1274
; Sequence 1274, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1274
;   LENGTH: 852
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1274

  Query Match             1.0%;  Score 20;  DB 4;  Length 852;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1467 GGCACGACCATTGCTTAACC 1486
              ||||||||||||||||||||
Db         56 GGCACGACCATTGCTTAACC 75


RESULT 5
US-09-252-991A-1381/c
; Sequence 1381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1381
;   LENGTH: 909
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1381

  Query Match             1.0%;  Score 20;  DB 4;  Length 909;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1467 GGCACGACCATTGCTTAACC 1486
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Db        112 GGCACGACCATTGCTTAACC 93


RESULT 6
US-09-252-991A-1287/c
; Sequence 1287, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1287
;   LENGTH: 1092
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1287

  Query Match             1.0%;  Score 20;  DB 4;  Length 1092;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1467 GGCACGACCATTGCTTAACC 1486
             ||||||||||||||||||||
Db        126 GGCACGACCATTGCTTAACC 107


RESULT 7
US-09-228-986-11
; Sequence 11, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
;  APPLICANT: Strabala, Timothy
;  APPLICANT: Nieuwenhuizen, Niels
;  TITLE OF INVENTION: Compositions Isolated from Plant Cells
;  TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
;  FILE REFERENCE: 11000/1020
;  CURRENT APPLICATION NUMBER: US/09/228,986
;  CURRENT FILING DATE: 1999-01-12
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
;   LENGTH: 3097
;   TYPE: DNA
;   ORGANISM: Eucalyptus grandis
US-09-228-986-11

  Query Match             1.0%;  Score 20;  DB 4;  Length 3097;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1387 GTTGTGCTTTTGGAGCTCAT 1406
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Db       2556 GTTGTGCTTTTGGAGCTCAT 2575


RESULT 8
US-09-800-729-18
; Sequence 18, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 5720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-800-729-18

  Query Match             1.0%;  Score 20;  DB 4;  Length 5720;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        667 CAACCTCCTCCACCTCCACC 686
              ||||||||||||||||||||
Db       5431 CAACCTCCTCCACCTCCACC 5450


RESULT 9
US-09-755-665-46/c
; Sequence 46, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
;  APPLICANT: Prayaga, Sudhirdas K.
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Taillon, Bruce E.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  MacDougall, John
;  TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 15966-631
;  CURRENT APPLICATION NUMBER: US/09/755,665
;  CURRENT FILING DATE:  2001-08-14
;  PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 41100
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GENOMIC DNA
US-09-755-665-46

  Query Match             1.0%;  Score 20;  DB 4;  Length 41100;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        921 TGGGAGTGGTCAGGGAGAGA 940
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Db      22048 TGGGAGTGGTCAGGGAGAGA 22029


RESULT 10
US-08-991-789A-168
; Sequence 168, Application US/08991789A
; Patent No. 6225054
;   GENERAL INFORMATION:
;        APPLICANT: Frudakis, Tony N.
;                   Smith, John M.
;                   Reed, Steven G.
;        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                            TREATMENT AND DIAGNOSIS OF BREAST CANCER
;        NUMBER OF SEQUENCES: 292
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Seed IP Law Group
;             STREET: 701 Fifth Avenue, Suite 6300
```

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;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/991,789A
;             FILING DATE: 11-Dec-1997
;             CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Potter, Jane E. R.
;             REGISTRATION NUMBER: 33,332
;             REFERENCE/DOCKET NUMBER: 210121.419C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 168:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 358 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 168:
US-08-991-789A-168

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  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        950 AGGCAGAGGTTGAGATCAT 968
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Db        228 AGGCAGAGGTTGAGATCAT 246


RESULT 11
US-09-062-451-168
; Sequence 168, Application US/09062451
; Patent No. 6344550
;  GENERAL INFORMATION:
;    APPLICANT:  Frudakis, Tony N.
;    APPLICANT:  Smith, John M.
;    APPLICANT:  Reed, Steven G.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;    NUMBER OF SEQUENCES:  297
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,451
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.419C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  168:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  358 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-062-451-168

  Query Match             1.0%;  Score 19;  DB 4;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        950 AGGCAGAGGTTGAGATCAT 968
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Db        228 AGGCAGAGGTTGAGATCAT 246


RESULT 12
US-09-598-326-168
; Sequence 168, Application US/09598326
; Patent No. 6423496
;  GENERAL INFORMATION:
;       APPLICANT: Frudakis, Tony N.
;                  Smith, John M.
;                  Reed, Steven G.
;       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;                           TREATMENT AND DIAGNOSIS OF BREAST CANCER
;       NUMBER OF SEQUENCES: 247
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group PLLC
;            STREET: 701 Fifth Avenue, Suite 6300
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/598,326
;            FILING DATE: 20-Jun-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Potter, Jane E.R.
;            REGISTRATION NUMBER: 33,332
;            REFERENCE/DOCKET NUMBER: 210121.419D1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 168:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 358 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 168:
US-09-598-326-168

  Query Match             1.0%;  Score 19;  DB 4;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        950 AGGCAGAGGTTGAGATCAT 968
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Db        228 AGGCAGAGGTTGAGATCAT 246


RESULT 13
US-09-289-198-168
; Sequence 168, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
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;  APPLICANT: Frudakis, Tony N.
;  APPLICANT: Smith, John M.
;  APPLICANT: Reed, Steven G.
;  APPLICANT: Misher, Lynda
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.419C5
;  CURRENT APPLICATION NUMBER: US/09/289,198
;  CURRENT FILING DATE: 1999-04-09
;  EARLIER APPLICATION NUMBER: US 09/062,451
;  EARLIER FILING DATE: 1998-04-17
;  EARLIER APPLICATION NUMBER: US 08/991,789
;  EARLIER FILING DATE: 1997-12-11
;  EARLIER APPLICATION NUMBER: US 08/838,762
;  EARLIER FILING DATE: 1997-04-09
;  EARLIER APPLICATION NUMBER: PCT/US97/00485
;  EARLIER FILING DATE: 1997-01-10
;  EARLIER APPLICATION NUMBER: US 08/700,014
;  EARLIER FILING DATE: 1996-08-20
;  EARLIER APPLICATION NUMBER: US 08/585,392
;  EARLIER FILING DATE: 1996-01-01
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 168
;   LENGTH: 358
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-289-198-168

  Query Match             1.0%;  Score 19;  DB 4;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        950 AGGCAGAGGTTGAGATCAT 968
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Db        228 AGGCAGAGGTTGAGATCAT 246


RESULT 14
US-09-429-755-168
; Sequence 168, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
;  APPLICANT:  Frudakis, Tony N.
;  APPLICANT:  Smith, John M.
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Misher, Lynda
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Dillon, Davin C.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.419C6
;  CURRENT APPLICATION NUMBER: US/09/429,755A
;  CURRENT FILING DATE:  1999-10-28
;  NUMBER OF SEQ ID NOS:  315
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 168
;   LENGTH: 358
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-429-755-168

  Query Match             1.0%;  Score 19;  DB 4;  Length 358;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        950 AGGCAGAGGTTGAGATCAT 968
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Db        228 AGGCAGAGGTTGAGATCAT 246


RESULT 15
US-09-187-330-4/c
; Sequence 4, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
;  APPLICANT: Gozes, Illana
;  APPLICANT: Brenneman, Douglas E.
;  APPLICANT: Bassan, Merav
;  APPLICANT: Zamostiano, Rachel
;  APPLICANT: The Government of the United States of America
;  APPLICANT: as represented by the Secretary of the
;  APPLICANT: Department of Health and Human Services
;  TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
;  FILE REFERENCE: 015280-291200US
;  CURRENT APPLICATION NUMBER: US/09/187,330
;  CURRENT FILING DATE: 1998-11-06
;  EARLIER APPLICATION NUMBER: US 60/037,404
;  EARLIER FILING DATE: 1997-02-07
;  EARLIER APPLICATION NUMBER: WO PCT/US98/02485
;  EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2421
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: one mouse activity dependent neurotrophic factor
;   OTHER INFORMATION: III (ADNF III) cDNA clone
US-09-187-330-4

  Query Match             1.0%;  Score 19;  DB 4;  Length 2421;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         69 TCCTCCTCCAGCTTCCGCT 87
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Db       1295 TCCTCCTCCAGCTTCCGCT 1277


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GenCore version 5.1.6
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Perfect score: 1944
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1944	100.0	2189	14	US-10-086-464-3	Sequence 3, Appli
3	26	1.3	268	9	US-09-923-876-5096	Sequence 5096, Ap
4	26	1.3	268	11	US-09-923-876-5096	Sequence 5096, Ap
5	26	1.3	951	13	US-10-425-114-1922	Sequence 1922, Ap
6	26	1.3	1011	13	US-10-425-114-13131	Sequence 13131, A
7	26	1.3	1134	13	US-10-425-114-36420	Sequence 36420, A
8	26	1.3	1500	13	US-10-425-114-6300	Sequence 6300, Ap
9	26	1.3	1552	13	US-10-424-599-47702	Sequence 47702, A
10	26	1.3	1724	13	US-10-425-114-2326	Sequence 2326, Ap
11	25	1.3	1101	13	US-10-424-599-122411	Sequence 122411,
12	24	1.2	1515	13	US-10-368-046-1	Sequence 1, Appli
13	24	1.2	1515	16	US-10-367-095-1	Sequence 1, Appli
14	23	1.2	180	15	US-10-029-386-26494	Sequence 26494, A
15	23	1.2	579	15	US-10-029-386-12794	Sequence 12794, A
16	23	1.2	897	16	US-10-106-938A-10	Sequence 10, Appl
17	23	1.2	897	16	US-10-106-938A-11	Sequence 11, Appl
18	23	1.2	897	16	US-10-106-938A-14	Sequence 14, Appl
19	23	1.2	1281	16	US-10-106-938A-12	Sequence 12, Appl
20	23	1.2	1289	15	US-10-378-393-21	Sequence 21, Appl
21	23	1.2	1939	13	US-10-424-599-1237	Sequence 1237, Ap
22	23	1.2	1987	15	US-10-378-393-17	Sequence 17, Appl
23	23	1.2	4517	16	US-10-093-463-117	Sequence 117, App
24	23	1.2	4586	10	US-09-983-000A-11	GENERAL INFORMATI
25	23	1.2	4586	15	US-10-102-524-1707	Sequence 1707, Ap
26	23	1.2	4620	16	US-10-106-938A-1	Sequence 1, Appli
27	23	1.2	4726	13	US-10-087-192-323	Sequence 323, App
28	23	1.2	144035	13	US-10-087-192-322	Sequence 322, App
29	21	1.1	1179	13	US-10-425-114-4027	Sequence 4027, Ap
30	21	1.1	1186	13	US-10-425-114-4273	Sequence 4273, Ap
31	21	1.1	2196	14	US-10-086-464-7	Sequence 7, Appli
32	21	1.1	2231	14	US-10-086-464-6	Sequence 6, Appli
33	21	1.1	822900	16	US-10-292-798-1393	Sequence 1393, Ap
c 34	20	1.0	213	9	US-09-867-701-9615	Sequence 9615, Ap
c 35	20	1.0	260	13	US-10-424-599-58928	Sequence 58928, A
36	20	1.0	432	13	US-09-770-423-122	Sequence 122, App
37	20	1.0	609	9	US-09-800-729-55	Sequence 55, Appl
c 38	20	1.0	623	13	US-10-425-114-4896	Sequence 4896, Ap
c 39	20	1.0	655	13	US-10-425-114-11463	Sequence 11463, A
c 40	20	1.0	727	13	US-10-412-699B-993	Sequence 993, App
c 41	20	1.0	727	16	US-10-374-780A-492	Sequence 492, App
c 42	20	1.0	751	13	US-10-425-114-4607	Sequence 4607, Ap
c 43	20	1.0	767	13	US-10-412-699B-995	Sequence 995, App
c 44	20	1.0	767	16	US-10-374-780A-494	Sequence 494, App
45	20	1.0	918	13	US-10-424-599-54382	Sequence 54382, A

ALIGNMENTS

RESULT 1
US-10-086-464-1
; Sequence 1, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1944)
US-10-086-464-1

Query Match 100.0%; Score 1944; DB 14; Length 1944;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60
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Db 1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60

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Qy       121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180
Db       121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180

Qy       181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240
Db       181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240

Qy       241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300
Db       241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300

Qy       301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360
Db       301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360

Qy       361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420
Db       361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420

Qy       421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480
Db       421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480

Qy       481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540
Db       481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540

Qy       541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
Db       541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600

Qy       601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660
Db       601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660

Qy       661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720
Db       661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720

Qy       721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780
Db       721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780

Qy       781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840
Db       781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840

Qy       841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900
Db       841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900

Qy       901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960
Db       901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960

Qy       961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
Db       961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020

Qy      1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080
Db      1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080

Qy      1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140
Db      1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140

Qy      1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200
Db      1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200

Qy      1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260
Db      1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

Qy      1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
Db      1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320

Qy      1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
Db      1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380

Qy      1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
Db      1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440

Qy      1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500
Db      1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500

Qy      1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
Db      1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560

Qy      1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
Db      1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620

Qy      1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
Db      1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680

Qy      1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740
Db      1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740

Qy      1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800
Db      1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800

Qy      1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
Db      1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860

Qy      1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920
Db      1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920

Qy      1921 GGTTATAGTGGACCTTCTCTTTAA 1944
Db      1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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RESULT 2
US-10-086-464-3
; Sequence 3, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
; APPLICANT: GORING, Daphne R. et al.
; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
; FILE REFERENCE: P 25,762-A USA
; CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: PCT/CA00/00966
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 60/159,122

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;  PRIOR FILING DATE: 1999-10-13
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2189
;   TYPE: DNA
;   ORGANISM: Brassica napus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2189)
;   OTHER INFORMATION:
US-10-086-464-3

  Query Match            100.0%;  Score 1944;  DB 14;  Length 2189;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1944;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCACA 156

Qy         61 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 ACCACCACTCCTCCTCCAGCTTCCGCTCCTCCTCCCACCACACCTTCTTCTCCTCCGCCG 216

Qy        121 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 CCATCCACTATTCCGACATCTCCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCCT 276

Qy        181 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 CCATCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCA 336

Qy        241 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CCCGCTCCAACTACGCCCGGATCTCCACCCGCACCTGTTACTCCTCCTACTCGAAACCCT 396

Qy        301 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CCACCTTCAGTCCCAGGACCACCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCT 456

Qy        361 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 CCATCTTCTCCCTCGCCGCCGTCTCCTTCTTCCGACGGTTTATCAACAGGAGTGGTGGTG 516

Qy        421 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GGAATCGCCATCGGAGGAGTCGCTCTGCTTGTGATAGTGACTCTGATTTGTCTCCTCTGT 576

Qy        481 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 AAGAAGAAACGACGGAGAGACGAAGAAGATGCTTACTATGTTCCTCCGCCACCTCCTCCT 636

Qy        541 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GGTCCCAAAGCCGGAGGACCTTACGGTGGACAGCAGCAACAATGGCGGCAACAAAACGCA 696

Qy        601 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        697 ACACCACCGTCAGATCATGTCGTGACGTCACTACCACCACCACCTAAGGCTCCATCTCCA 756

Qy        661 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 CCACGGCAACCTCCTCCACCTCCACCACCGCCTTTCATGAGCAGCAGCGGCGGCTCCGAC 816

Qy        721 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TACTCGGACCGTCCAGTTCTTCCTCCACCGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAA 876

Qy        781 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 AGCACTTTCACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTG 936

Qy        841 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 TTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTT 996

Qy        901 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 GCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTT 1056

Qy        961 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 GAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCC 1116

Qy       1021 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 GGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTC 1176

Qy       1081 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 CATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1236

Qy       1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATC 1296

Qy       1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1356

Qy       1261 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 GCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG 1416

Qy       1321 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1476

Qy       1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTC 1536

Qy       1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA 1596

Qy       1501 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 GGAGACTTTGAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATG 1656

Qy       1561 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 GCTCGCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1716

Qy       1621 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 ATGAGCCAGATTGTGCGTGCGTTAGAAGGAAATGTATCACTGTCAGATCTTAACGAAGGG 1776

Qy       1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1777 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1836

Qy       1741 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1837 AGCCAGTACAATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC 1896

Qy       1801 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1897 AACGCCACGGGTGAGTACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCA 1956

Qy       1861 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1957 AGCAGCGAGGGCCAAACCACACGCGAAATGGAGATGGGGAAGATTAAGAGAACCGGTCAG 2016

Qy       1921 GGTTATAGTGGACCTTCTCTTTAA 1944
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Db       2017 GGTTATAGTGGACCTTCTCTTTAA 2040


RESULT 3
US-09-923-876-5096
; Sequence 5096, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
;  APPLICANT: Lalgudi, Raghunath V.
;  APPLICANT:  Kamigaki, Laura Y. (Ito)
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
;  FILE REFERENCE: PL-0012-1 CON
;  CURRENT APPLICATION NUMBER: US/09/923,876
;  CURRENT FILING DATE:  2001-08-06
;  PRIOR APPLICATION NUMBER: 09/298,329
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/085,331
;  PRIOR FILING DATE: 1998-05-05
;  NUMBER OF SEQ ID NOS: 6332
;  SOFTWARE: PERL Program
; SEQ ID NO 5096
;   LENGTH: 268
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020013958A1 700456354H1
;   NAME/KEY: unsure
;   LOCATION: 63
;   OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5096

  Query Match             1.3%;  Score 26;  DB 9;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 0.0045;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
             ||||||||||||||||||||||||||
Db        203 TTTGAAGCTAAGGTTGCTGATTTTGG 228


RESULT 4
US-09-923-876-5096
; Sequence 5096, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
;  APPLICANT: Lalgudi, Raghunath V.
;  APPLICANT:  Kamigaki, Laura Y. (Ito)
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
;  FILE REFERENCE: PL-0012-1 CON
;  CURRENT APPLICATION NUMBER: US/09/923,876
;  CURRENT FILING DATE:  2001-08-06
;  PRIOR APPLICATION NUMBER: 09/298,329
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/085,331
;  PRIOR FILING DATE: 1998-05-05
;  NUMBER OF SEQ ID NOS: 6332
;  SOFTWARE: PERL Program
; SEQ ID NO 5096
;   LENGTH: 268
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030237110A9 700456354H1
;   NAME/KEY: unsure
;   LOCATION: 63
;   OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5096

  Query Match             1.3%;  Score 26;  DB 11;  Length 268;
  Best Local Similarity   100.0%;  Pred. No. 0.0045;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
             ||||||||||||||||||||||||||
Db        203 TTTGAAGCTAAGGTTGCTGATTTTGG 228


RESULT 5
US-10-425-114-1922
; Sequence 1922, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1922
;   LENGTH: 951
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700171392_FLI
US-10-425-114-1922

  Query Match             1.3%;  Score 26;  DB 13;  Length 951;
  Best Local Similarity   100.0%;  Pred. No. 0.0046;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
             ||||||||||||||||||||||||||
Db          16 TTTGAAGCTAAGGTTGCTGATTTTGG 41


RESULT 6
US-10-425-114-13131
; Sequence 13131, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13131
;   LENGTH: 1011
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: JC-GMFL02220096D10_FLI
US-10-425-114-13131

  Query Match             1.3%;  Score 26;  DB 13;  Length 1011;
  Best Local Similarity   100.0%;  Pred. No. 0.0046;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1360 GAGAAGTCTGACGTTTTCTCATTTGG 1385
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Db        246 GAGAAGTCTGACGTTTTCTCATTTGG 271


RESULT 7
US-10-425-114-36420
; Sequence 36420, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 36420
;   LENGTH: 1134
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mexicana
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE097B02_FLI
US-10-425-114-36420

  Query Match             1.3%;  Score 26;  DB 13;  Length 1134;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
                ||||||||||||||||||||||||||
Db        260 TTTGAAGCTAAGGTTGCTGATTTTGG 285


RESULT 8
US-10-425-114-6300
; Sequence 6300, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6300
;   LENGTH: 1500
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700560157_FLI
US-10-425-114-6300

  Query Match             1.3%;  Score 26;  DB 13;  Length 1500;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1360 GAGAAGTCTGACGTTTTCTCATTTGG 1385
                ||||||||||||||||||||||||||
Db        779 GAGAAGTCTGACGTTTTCTCATTTGG 804


RESULT 9
US-10-424-599-47702
; Sequence 47702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 47702
;   LENGTH: 1552
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_143080C.1
US-10-424-599-47702

  Query Match             1.3%;  Score 26;  DB 13;  Length 1552;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1360 GAGAAGTCTGACGTTTTCTCATTTGG 1385
                ||||||||||||||||||||||||||
Db        779 GAGAAGTCTGACGTTTTCTCATTTGG 804


RESULT 10
US-10-425-114-2326
; Sequence 2326, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2326
;   LENGTH: 1724
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700209610_FLI
US-10-425-114-2326

  Query Match             1.3%;  Score 26;  DB 13;  Length 1724;
  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1231 TTTGAAGCTAAGGTTGCTGATTTTGG 1256
                ||||||||||||||||||||||||||
Db        832 TTTGAAGCTAAGGTTGCTGATTTTGG 857


RESULT 11
US-10-424-599-122411
; Sequence 122411, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
```

```
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 122411
;   LENGTH: 1101
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_81542C.1
US-10-424-599-122411

  Query Match             1.3%;  Score 25;  DB 13;  Length 1101;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1178 CTAAAATCATTCACCGTGATATCAA 1202
             |||||||||||||||||||||||||
Db         69 CTAAAATCATTCACCGTGATATCAA 93


RESULT 12
US-10-368-046-1
; Sequence 1, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
;  APPLICANT: Robin A. Robinson
;  APPLICANT:  Vittoria Cioce
;  TITLE OF INVENTION: Method for Isolation and Purification of
;  TITLE OF INVENTION:  Expressed Gene Products In Vitro
;  FILE REFERENCE: 44149-3US1
;  CURRENT APPLICATION NUMBER: US/10/368,046
;  CURRENT FILING DATE:  2003-02-15
;  PRIOR APPLICATION NUMBER: US 60/356,119
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,161
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,118
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,133
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,157
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,156
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,123
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,113
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,154
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,135
;  PRIOR FILING DATE: 2002-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1515
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HPV-16 L1 codon optimized sequence
US-10-368-046-1

  Query Match             1.2%;  Score 24;  DB 13;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
              ||||||||||||||||||||||||
Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 13
US-10-367-095-1
; Sequence 1, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
;  APPLICANT: Robin A. Robinson
;  TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line
;  FILE REFERENCE: 44149-1US1
;  CURRENT APPLICATION NUMBER: US/10/367,095
;  CURRENT FILING DATE:  2003-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,119
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,161
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,118
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,133
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,157
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,156
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,123
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,113
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,154
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,135
;  PRIOR FILING DATE: 2002-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1515
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HPV-16 L1 codon optimized sequence
US-10-367-095-1

  Query Match             1.2%;  Score 24;  DB 16;  Length 1515;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACCTCCTCCACCTCCACCACCGCC 692
              ||||||||||||||||||||||||
Db       1471 ACCTCCTCCACCTCCACCACCGCC 1494


RESULT 14
US-10-029-386-26494
; Sequence 26494, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26494
;   LENGTH: 180
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
```

```
;   OTHER INFORMATION: MAP TO CHR7.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
;   OTHER INFORMATION: SWISSPROT HIT: P16056, EVALUE 1.00e-27
;   OTHER INFORMATION: NT HIT: gi4557746, EVALUE 8.00e-90
;   OTHER INFORMATION: EST_HUMAN HIT: AW418529.1, EVALUE 8.00e-97
US-10-029-386-26494

  Query Match             1.2%;  Score 23;  DB 15;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.2;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 AAGGTTGCTGATTTTGGTCTTGC 1262
              |||||||||||||||||||||||
Db         29 AAGGTTGCTGATTTTGGTCTTGC 51


RESULT 15
US-10-029-386-12794
; Sequence 12794, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12794
;   LENGTH: 579
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO CHR7.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.59
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
;   OTHER INFORMATION: NT HIT: U96996.1, EVALUE 1.00e-107
;   OTHER INFORMATION: SWISSPROT HIT: P16056, EVALUE 6.00e-27
;   OTHER INFORMATION: EST_HUMAN HIT: AW418529.1, EVALUE 0.00e+00
US-10-029-386-12794

  Query Match             1.2%;  Score 23;  DB 15;  Length 579;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1240 AAGGTTGCTGATTTTGGTCTTGC 1262
              |||||||||||||||||||||||
Db        221 AAGGTTGCTGATTTTGGTCTTGC 243


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Job time : 843 secs
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